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1 GACAGAGTGCAGCCTTTTCAGACTCTGTGACACAGTTCCCCTTTT  
 46 GCAAAAATACTTAGCGAGGATCATTACTTTCCAACAGTCGTGTCC  
 91 AGAGACCTACTTTTGTAACACCGCAGGGAAGTTAATGTACTAGGTC  
 136 TTGAAAGGTCTTTCTGGAATGTGCAGTAACTTGTAAGTTTCTTCT  
 181 AGTAGCACTGCTAATTTTTTGTGTTATAATTTTTTGTAGGTCCATGG  
  
 226 GGCCGATGTATGGGAGATGAATGTGGTCCCGGAGGCATCCAAACG  
     MetGlyAspGluCysGlyProGlyGlyIleGlnThr  
  
 271 AGGGCTGTGTGGTGTGCTCATGTGGAGGGATGGACTACACTGCAT  
     ArgAlaValTrpCysAlaHisValGluGlyTrpThrThrLeuHis  
  
 316 ACTAACTGTAAGCAGGCCGAGAGACCCAATAACCAGCAGAATTGT  
     ThrAsnCysLysGlnAlaGluArgProAsnAsnGlnGlnAsnCys  
  
 361 TTCAAAGTTTGCGATTGGCACAAAGAGTTGTACGACTGGAGACTG  
     PheLysValCysAspTrpHisLysGluLeuTyrAspTrpArgLeu  
  
 406 GGACCTTGGAATCAGTGTGAGCCCGTGATTTCAAAAAGCCTAGAG  
     GlyProTrpAsnGlnCysGlnProValIleSerLysSerLeuGlu  
  
 451 AAACCTCTTGAGTGCATTAAGGGGGAAGAAGGTATTCAGGTGAGG  
     LysProLeuGluCysIleLysGlyGluGluGlyIleGlnValArg  
  
 496 GAGATAGCGTGCATCCAGAAAGACAAAGACATTCCTGCGGAGGAT  
     GluIleAlaCysIleGlnLysAspLysAspIleProAlaGluAsp  
  
 541 ATCATCTGTGAGTACTTTGAGCCCAAGCCTCTCCTGGAGCAGGCT  
     IleIleCysGluTyrPheGluProLysProLeuLeuGluGlnAla  
  
 586 TGCCTCATTCCTTGCCAGCAAGATTGCATCGTGTCTGAATTTTCT  
     CysLeuIleProCysGlnGlnAspCysIleValSerGluPheSer  
  
 631 GCCTGGTCCGAATGCTCCAAGACCTGCGGCAGCGGGCTCCAGCAC  
     AlaTrpSerGluCysSerLysThrCysGlySerGlyLeuGlnHis  
  
 676 CGGACGCGTCATGTGGTGGCGCCCCCGCAGTTCGGAGGCTCTGGC  
     ArgThrArgHisValValAlaProProGlnPheGlyGlySerGly  
  
 721 TGTCCAAACCTGACGGAGTTCAGGTGTGCCAATCCAGTCCATGC  
     CysProAsnLeuThrGluPheGlnValCysGlnSerSerProCys  
  
 766 GAGGCCGAGGAGCTCAGGTACAGCCTGCATGTGGGGCCCTGGAGC  
     GluAlaGluGluLeuArgTyrSerLeuHisValGlyProTrpSer  
  
 811 ACCTGCTCAATGCCCCACTCCCGACAAGTAAGACAAGCAAGGAGA  
     ThrCysSerMetProHisSerArgGlnValArgGlnAlaArgArg

Fig 1

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856 CGCGGGAAGAATAAAGAACGGGAAAAGGACCGCAGCAAAGGAGTA  
ArgGlyLysAsnLysGluArgGluLysAspArgSerLysGlyVal

901 AAGGATCCAGAAGCCCGCGAGCTTATTAAGAAAAAGAGAAACAGA  
LysAspProGluAlaArgGluLeuIleLysLysLysArgAsnArg

946 AACAGGCAGAACAGACAAGAGAACAAATATTGGGACATCCAGATT  
AsnArgGlnAsnArgGlnGluAsnLysTyrTrpAspIleGlnIle

991 GGATATCAGACCAGAGAGGTTATGTGCATTAACAAGACGGGGAAA  
GlyTyrGlnThrArgGluValMetCysIleAsnLysThrGlyLys

1036 GCTGCTGATTTAAGCTTTTGCCAGCAAGAGAAGCTTCCAATGACC  
AlaAlaAspLeuSerPheCysGlnGlnGluLysLeuProMetThr

1081 TTCCAGTCCTGTGTGATCACCAAAGAGTGCCAGGTTTCCGAGTGG  
PheGlnSerCysValIleThrLysGluCysGlnValSerGluTrp

1126 TCAGAGTGGAGCCCCTGCTCAAAAACATGCCATGACATGGTGTCC  
SerGluTrpSerProCysSerLysThrCysHisAspMetValSer

1171 CCTGCAGGCACTCGTGTAAGGACACGAACCATCAGGCAGTTTCCC  
ProAlaGlyThrArgValArgThrArgThrIleArgGlnPhePro

1216 ATTGGCAGTGAAAAGGAGTGTCCAGAATTTGAAGAAAAAGAACCC  
IleGlySerGluLysGluCysProGluPheGluGluLysGluPro

1261 TGTTTGTCTCAAGGAGATGGAGTTGTCCCCTGTGCCACGTATGGC  
CysLeuSerGlnGlyAspGlyValValProCysAlaThrTyrGly

1306 TGGAGAACTACAGAGTGGACTGAGTGCCGTGTGGACCCTTTGCTC  
TrpArgThrThrGluTrpThrGluCysArgValAspProLeuLeu

1351 AGTCAGCAGGACAAGAGGCGCGGCAACCAGACGGCCCTCTGTGGA  
SerGlnGlnAspLysArgArgGlyAsnGlnThrAlaLeuCysGly

1396 GGGGGCATCCAGACCCGAGAGGTGTACTGCGTGCAGGCCAACGAA  
GlyGlyIleGlnThrArgGluValTyrCysValGlnAlaAsnGlu

1441 AACCTCCTCTCACAATTAAGTACCCACAAGAACAAAGAAGCCTCA  
AsnLeuLeuSerGlnLeuSerThrHisLysAsnLysGluAlaSer

1486 AAGCCAATGGACTTAAATTAATGCACTGGACCTATCCCTAATACT  
LysProMetAspLeuLysLeuCysThrGlyProIleProAsnThr

1531 ACACAGCTGTGCCACATTTCCTTGTCCTCAACTGAATGTGAAGTTTCA  
ThrGlnLeuCysHisIleProCysProThrGluCysGluValSer

Fig 1 (continued)

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1576 CCTTGGTCAGCTTGGGGACCTTGTACTTATGAAAACCTGTAATGAT  
ProTrpSerAlaTrpGlyProCysThrTyrGluAsnCysAsnAsp

1621 CAGCAAGGGAAAAAAGGCTTCAAACCTGAGGAAGCGGCGCATTACC  
GlnGlnGlyLysLysGlyPheLysLeuArgLysArgArgIleThr

1666 AATGAGCCCACTGGAGGCTCTGGGGTAACCGGAAACCTGCCCTCAC  
AsnGluProThrGlyGlySerGlyValThrGlyAsnCysProHis

1711 TTACTGGAAGCCATTCCCTGTGAAGAGCCTGCCTGTTATGACTGG  
LeuLeuGluAlaIleProCysGluGluProAlaCysTyrAspTrp

1756 AAAGCGGTGAGACTGGGAGACTGCGAGCCAGATAACGGAAAGGAG  
LysAlaValArgLeuGlyAspCysGluProAspAsnGlyLysGlu

1801 TGTGGTCCAGGCACGCAAGTTCAAGAGGTTGTGTGCATCAACAGT  
CysGlyProGlyThrGlnValGlnGluValValCysIleAsnSer

1846 GATGGAGAAGAAGTTGACAGACAGCTGTGCAGAGATGCCATCTTC  
AspGlyGluGluValAspArgGlnLeuCysArgAspAlaIlePhe

1891 CCCATCCCTGTGGCCTGTGATGCCCCATGCCCGAAAGACTGTGTG  
ProIleProValAlaCysAspAlaProCysProLysAspCysVal

1936 CTCAGCACATGGTCTACGTGGTCCTCCTGCTCACACACCTGCTCA  
LeuSerThrTrpSerThrTrpSerSerCysSerHisThrCysSer

1981 GGGAAAACGACAGAAGGGAAACAGATACGAGCACGATCCATTCTG  
GlyLysThrThrGluGlyLysGlnIleArgAlaArgSerIleLeu

2026 GCCTATGCGGGTGAAGAAGGTGGAATTCGCTGTCCAAATAGCAGT  
AlaTyrAlaGlyGluGluGlyGlyIleArgCysProAsnSerSer

2071 GCTTTGCAAGAAGTACGAAGCTGTAATGAGCATCCTTGACACAGTG  
AlaLeuGlnGluValArgSerCysAsnGluHisProCysThrVal

2116 TACCACTGGCAAACCTGGTCCCTGGGGCCAGTGCATTGAGGACACC  
TyrHisTrpGlnThrGlyProTrpGlyGlnCysIleGluAspThr

2161 TCAGTATCGTCCTTCAACACAACCTACGACTTGGAATGGGGAGGCC  
SerValSerSerPheAsnThrThrThrThrTrpAsnGlyGluAla

2206 TCCTGCTCTGTCTGGCATGCAGACAAGAAAAGTCATCTGTGTGCGA  
SerCysSerValGlyMetGlnThrArgLysValIleCysValArg

2251 GTCAATGTGGGCCAAGTGGGACCCAAAAAATGTCCTGAAAGCCTT  
ValAsnValGlyGlnValGlyProLysLysCysProGluSerLeu

Fig 1 (continued)

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2296 CGACCTGAAACTGTAAGGCCTTGTCTGCTTCCTTGTAAGAAGGAC  
ArgProGluThrValArgProCysLeuLeuProCysLysLysAsp

2341 TGTATTGTGACCCCATATAGTGACTGGACATCATGCCCTCTTCG  
CysIleValThrProTyrSerAspTrpThrSerCysProSerSer

2386 TGTAAGAAGGGGACTCCAGTATCAGGAAGCAGTCTAGGCATCGG  
CysLysGluGlyAspSerSerIleArgLysGlnSerArgHisArg

2431 GTCATCATTCAGCTGCCAGCCAACGGGGGCCGAGACTGCACAGAT  
ValIleIleGlnLeuProAlaAsnGlyGlyArgAspCysThrAsp

2476 CCCCTCTATGAAGAGAAGGCCTGTGAGGCACCTCAAGCGTGCCAA  
ProLeuTyrGluGluLysAlaCysGluAlaProGlnAlaCysGln

2521 AGCTACAGGTGGAAGACTCACAAATGGCGCAGATGCCAATTAGTC  
SerTyrArgTrpLysThrHisLysTrpArgArgCysGlnLeuVal

2566 CCTTGGAGCGTGCAACAAGACAGCCCTGGAGCACAGGAAGGCTGT  
ProTrpSerValGlnGlnAspSerProGlyAlaGlnGluGlyCys

2611 GGGCCTGGGCGACAGGCAAGAGCCATTACTTGTCGCAAGCAAGAT  
GlyProGlyArgGlnAlaArgAlaIleThrCysArgLysGlnAsp

2656 GGAGGACAGGCTGGAATCCATGAGTGCCTACAGTATGCAGGCCCT  
GlyGlyGlnAlaGlyIleHisGluCysLeuGlnTyrAlaGlyPro

2701 GTGCCAGCCCTTACCCAGGCCTGCCAGATCCCCTGCCAGGATGAC  
ValProAlaLeuThrGlnAlaCysGlnIleProCysGlnAspAsp

2746 TGTCAATTGACCAGCTGGTCCAAGTTTTCTTCATGCAATGGAGAC  
CysGlnLeuThrSerTrpSerLysPheSerSerCysAsnGlyAsp

2791 TGTGGTGCAGTTAGGACCAGAAAGCGCACTCTTGTTGGAAAAAGT  
CysGlyAlaValArgThrArgLysArgThrLeuValGlyLysSer

2836 AAAAAGAAGGAAAAATGTAAAAATTCCCATTTGTATCCCCTGATT  
LysLysLysGluLysCysLysAsnSerHisLeuTyrProLeuIle

2881 GAGACTCAGTATTGTCCTTGTGACAAATATAATGCACAACCTGTG  
GluThrGlnTyrCysProCysAspLysTyrAsnAlaGlnProVal

2926 GGGAAGTGGTCAGACTGTATTTTACCAGAGGGAAAAGTGGAAGTG  
GlyAsnTrpSerAspCysIleLeuProGluGlyLysValGluVal

2971 TTGCTGGGAATGAAAGTACAAGGAGACATCAAGGAATGCGGACAA  
LeuLeuGlyMetLysValGlnGlyAspIleLysGluCysGlyGln

Fig 1 (continued)

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3016 GGATATCGTTACCAAGCAATGGCATGCTACGATCAAAATGGCAGG  
 GlyTyrArgTyrGlnAlaMetAlaCysTyrAspGlnAsnGlyArg  
 3061 CTTGTGGAAACATCTAGATGTAACAGCCATGGTTACATTGAGGAG  
 LeuValGluThrSerArgCysAsnSerHisGlyTyrIleGluGlu  
 3106 GCCTGCATCATCCCCTGCCCTCAGACTGCAAGCTCAGTGAGTGG  
 AlaCysIleIleProCysProSerAspCysLysLeuSerGluTrp  
 3151 TCCAAC TGGTCGCGCTGCAGCAAGTCCTGTGGGAGTGGTGTGAAG  
 SerAsnTrpSerArgCysSerLysSerCysGlySerGlyValLys  
 3196 GTTCGTTCTAAATGGCTGCGTGAAAAACCATATAATGGAGGAAGG  
 ValArgSerLysTrpLeuArgGluLysProTyrAsnGlyGlyArg  
 3241 CCTTGCCCCAAACTGGACCATGTCAACCAGGCACAGGTGTATGAG  
 ProCysProLysLeuAspHisValAsnGlnAlaGlnValTyrGlu  
 3286 GTTGTCCCATGCCACAGTGACTGCAACCAGTACCTATGGGTCACA  
 ValValProCysHisSerAspCysAsnGlnTyrLeuTrpValThr  
 3331 GAGCCCTGGAGCATCTGCAAGGTGACCTTTGTGAATATGCGGGAG  
 GluProTrpSerIleCysLysValThrPheValAsnMetArgGlu  
 3376 AACTGTGGAGAGGGCGTGCAAACCCGAAAAGTGAGATGCATGCAG  
 AsnCysGlyGluGlyValGlnThrArgLysValArgCysMetGln  
 3421 AATACAGCAGATGGCCCTTCTGAACATGTAGAGGATTACCTCTGT  
 AsnThrAlaAspGlyProSerGluHisValGluAspTyrLeuCys  
 3466 GACCCAGAAGAGATGCCCTGGGCTCTAGAGTGTGCAAATTACCA  
 AspProGluGluMetProLeuGlySerArgValCysLysLeuPro  
 3511 TGCCCTGAGGACTGTGTGATATCTGAATGGGGTCCATGGACCCAA  
 CysProGluAspCysValIleSerGluTrpGlyProTrpThrGln  
 3556 TGTGTTTTGCCTTGCAATCAAAGCAGTTTCCGGCAAAGGTCAGCT  
 CysValLeuProCysAsnGlnSerSerPheArgGlnArgSerAla  
 3601 GATCCCATCAGACAACCAGCTGATGAAGGAAGATCTTGCCCTAAT  
 AspProIleArgGlnProAlaAspGluGlyArgSerCysProAsn  
 3646 GCTGTTGAGAAAGAACCCTGTAACCTGAACAAAAACTGCTACCAC  
 AlaValGluLysGluProCysAsnLeuAsnLysAsnCysTyrHis  
 3691 TATGATTATAATGTAACAGACTGGAGTACATGTCAGCTGAGTGAG  
 TyrAspTyrAsnValThrAspTrpSerThrCysGlnLeuSerGlu

Fig 1 (continued)

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3736 AAGGCAGTTTGTGGAAATGGAATAAAAACAAGGATGTTGGATTGT  
LysAlaValCysGlyAsnGlyIleLysThrArgMetLeuAspCys

3781 GTTCGAAGTGATGGCAAGTCAGTTGACCTGAAATATTGTGAAGCG  
ValArgSerAspGlyLysSerValAspLeuLysTyrCysGluAla

3826 CTTGGCTTGGAGAAGAAGTGGCAGATGAACACGTCCTGCATGGTG  
LeuGlyLeuGluLysAsnTrpGlnMetAsnThrSerCysMetVal

3871 GAATGCCCTGTGAACTGTCAGCTTTCTGATTGGTCTCCTTGGTCA  
GluCysProValAsnCysGlnLeuSerAspTrpSerProTrpSer

3916 GAATGTTCTCAAACATGTGGCCTCACAGGAAAAATGATCCGAAGA  
GluCysSerGlnThrCysGlyLeuThrGlyLysMetIleArgArg

3961 CGAACAGTGACCCAGCCCTTTCAAGGTGATGGAAGACCATGCCCT  
ArgThrValThrGlnProPheGlnGlyAspGlyArgProCysPro

4006 TCCCTGATGGACCAGTCCAAACCCTGCCCAGTGAAGCCTTGTAT  
SerLeuMetAspGlnSerLysProCysProValLysProCysTyr

4051 CGGTGGCAATATGGCCAGTGGTCTCCATGCCAAGTGCAGGAGGCC  
ArgTrpGlnTyrGlyGlnTrpSerProCysGlnValGlnGluAla

4096 CAGTGTGGAGAAGGGACCAGAACAAGGAACATTTCTTGTGTAGTA  
GlnCysGlyGluGlyThrArgThrArgAsnIleSerCysValVal

4141 AGTGATGGGTCAGCTGATGATTTTCAGCAAAGTGGTGGATGAGGAA  
SerAspGlySerAlaAspAspPheSerLysValValAspGluGlu

4186 TTCTGTGCTGACATTGAACTCATTATAGATGGTAATAAAAATATG  
PheCysAlaAspIleGluLeuIleIleAspGlyAsnLysAsnMet

4231 GTTCTGGAGGAATCCTGCAGCCAGCCTTGCCCAGGTGACTGTTAT  
ValLeuGluGluSerCysSerGlnProCysProGlyAspCysTyr

4276 TTGAAGGACTGGTCTTCCTGGAGCCTGTGTCAGCTGACCTGTGTG  
LeuLysAspTrpSerSerTrpSerLeuCysGlnLeuThrCysVal

4321 AATGGTGAGGATCTAGGCTTTGGTGGAAATACAGGTCAGATCCAGA  
AsnGlyGluAspLeuGlyPheGlyGlyIleGlnValArgSerArg

4366 CCGGTGATTATACAAGAACTAGAGAATCAGCATCTGTGCCCAGAG  
ProValIleIleGlnGluLeuGluAsnGlnHisLeuCysProGlu

4411 CAGATGTTAGAAACAAAATCATGTTATGATGGACAGTGCTATGAA  
GlnMetLeuGluThrLysSerCysTyrAspGlyGlnCysTyrGlu

4456 TATAAATGGATGGCCAGTGCTTGGAAAGGGCTCTTCCCGAACAGTG  
TyrLysTrpMetAlaSerAlaTrpLysGlySerSerArgThrVal

Fig 1 (continued)

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4501 TGGTGTCAAAGGTCAGATGGTATAAATGTAACAGGGGGCTGCTTG  
TrpCysGlnArgSerAspGlyIleAsnValThrGlyGlyCysLeu

4546 GTGATGAGCCAGCCTGATGCCGACAGGTCTTGTAACCCACCGTGT  
ValMetSerGlnProAspAlaAspArgSerCysAsnProProCys

4591 AGTCAACCCCACTCGTACTGTAGCGAGACAAAAACATGCCATTGT  
SerGlnProHisSerTyrCysSerGluThrLysThrCysHisCys

4636 GAAGAAGGGTACACTGAAGTCATGTCTTCTAACAGCACCCCTTGAG  
GluGluGlyTyrThrGluValMetSerSerAsnSerThrLeuGlu

4681 CAATGCACACTTATCCCCGTGGTGGTATTACCCACCATGGAGGAC  
GlnCysThrLeuIleProValValValLeuProThrMetGluAsp

4726 AAAAGAGGAGATGTGAAAACCAGTCGGGCTGTACATCCAACCCAA  
LysArgGlyAspValLysThrSerArgAlaValHisProThrGln

4771 CCCTCCAGTAACCCAGCAGGACGGGGAAGGACCTGGTTTCTACAG  
ProSerSerAsnProAlaGlyArgGlyArgThrTrpPheLeuGln

4816 CCATTTGGGCCAGATGGGAGACTAAAGACCTGGGTTTACGGTGTA  
ProPheGlyProAspGlyArgLeuLysThrTrpValTyrGlyVal

4861 GCAGCTGGGGCATTGTGTTACTCATCTTTATTGTCTCCATGATT  
AlaAlaGlyAlaPheValLeuLeuIlePheIleValSerMetIle

4906 TATCTAGCTTGCAAAAAGCCAAAGAAACCCCAAAGAAGGCAAAAC  
TyrLeuAlaCysLysLysProLysLysProGlnArgArgGlnAsn

4951 AACCGACTGAAACCTTTAACCTTAGCCTATGATGGAGATGCCGAC  
AsnArgLeuLysProLeuThrLeuAlaTyrAspGlyAspAlaAsp

4996 ATGTAACATATAACTTTTCCTGGCAACAACCAGTTTCGGCTTTCT  
Met

Fig 1 (continued)

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5041 GACTTCATAGATGTCCAGAGGCCACAACAAATGTATCCAAACTGT  
5086 GTGGATTAAAAATATATTTTAATTTTAAAAATGGCATCATAAAGA  
5131 CAAGAGTGAAAATCATACTGCCACTGGAGATATTTAAGACAGTAC  
5176 CACTTATATACAGACCATCAACCGTGAGAATTATAGGAGATTTAG  
5221 CTGAATACATGCTGCATTCTGAAAGTTTTATGTCATCTTTTCTGA  
5266 AATCTACCGACTGAAAAACCACTTTCATCTCTAAAAAATAATGGT  
5311 GGAATTGGCCAGTTAGGATGCCTGATACAAGACCGTCTGCAGTGT  
5356 TAATCCATAAACTTCCTAGCATGAAGAGTTTCTACCAAGATCTC  
5401 CACAATACTATGGTCAAATTAACATGTGTACTCAGTTGAATGACA  
5446 CACATTATGTCAGATTATGTACTTGCTAATAAGCAATTTTAACAA  
5491 TGCATAACAAATAAACTCTAAGCTAAGCAGAAAATCCACTGAATA  
5536 AATTCAGCATCTTGGTGGTGCATGGTAGATTTTATTGACCTGCAT  
5581 TTCAGAGACAAAGCCTCTTTTTTAAGACTTCTTGTCTCTCTCCAA  
5626 AGTAAGAATGCTGGACAAGTACTAGTGTCTTAGAAGAACGAGTCC  
5671 TCAAGTTCAGTATTTTATAGTGGTAATTGTCTGGAAAACATAATTT  
5716 ACTTGTGTTAATAACAATACGTTTCTACTTTCCCTGATTTTCAAAC  
5761 TGGTTGCCTGCATCTTTTTTGTCTATATGGAAGGCACATTTTGTCA  
5806 CTATATTAGTGCAGCACGATAGGCGCTTAACCAGTATTGCCATAG  
5851 AAACGCTCTTTTTCATGTGGGATGAAGACATCTGTGCCAAGAGT  
5896 GGCATGAAGACATTTGCAAGTTCTTGTATCCTGAAGAGAGTAAAG  
5941 TTCAGTTTGGATGGCAGCAAGATGAAATCAGCTATTACACCTGCT  
5986 GTACACACACTTCCTCATCACTGCAGCCATTGTGAAATTGACAAC  
6031 ATGGCGGTAATTTAAGTGTTGAAGTCCCTAACCCCTTAACCCTCT  
6076 AAAAGGTGGATTCCCTCTAGTTGGTTTGTAATTGTTCTTTGAAGGC  
6121 TGTTTATGACTAGATTTTATATTTGTTATCTTTGTTAAGAAAAA  
6166 AAAAAGAAAAAGGAACTGGATGTCTTTTAAATTTTGAGCAGATGG  
6211 AGAAAAATAAATAATGTATCAATGACCTTTGTAATAAAGGAAAAA  
6256 AAAAAAAAATGTGGATTTTCTCTCTCTGATTTCCAGTTTCA  
6301 GATTGAATGTCTGTCTTGCAGGCAGTTATTTCAAATCCATAGTC  
6346 TTTNGCCTTCTCACTGGCAAAATTTGA

Fig 1 (continued)



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1 CACCCCTCTGCCTGCCCCAGCCCGCCCATCGCTTCCCCTTTGGAG  
 46 CCTCCTGCTGGGCCACTGGCTGGGATCAGGACACCAGTGATGGTA  
 91 AGTGCTGGCCCAGACTGAAGCTCGGAGAGGCACTCTGCTTGCCCA  
 136 GCGTCACAGTCTTAGCTCCCAACTGTCCTGGCTTCCAGTCTCCCT  
 181 TGCTTCCCAGATCCCAGACTCTAGCCCCAGCCCCGTCTCTTTCAC  
 226 CAGCTCCTGGGACCCTACGCAATCTGCGCCTGCGTCTCATCAGTC  
 271 GCCCCACATGTAACGTATCTACAACCAGCTGCACCAGCGACACC  
 316 TGTCCAACCCGGCCCCGGCCTGGGATGCTATGTGGGGGCCCCCAGC  
 361 CTGGGGTGCAGGGCCCCCTGTCAGGTCTGATAGGGAGAAGAGAAGG  
 406 AGCAGAAGGGGAGGGGCCTAACCCTGGGCTGGGGGTGGACTCAC  
 451 AGGACTGGGGGAAAGAGCTGCAATCAGAGGGTGTCTGCCATAGCT  
 496 GGGCTCAGGCATCTGTCCTTGGCTTTGTTGCCTGGCTCCAGGGAG  
 541 ATTCCGGGGGCCCTGTGCTGTGCCTCGAGCCTGACGGACACTGGG  
 586 TTCAGGCTGGCATCATCAGCTTTGCATCAAGCTGTGCCCAGGAGG  
 631 ACGCTCCTGTGCTGCTGACCAACACAGCTGCTCACAGTTCCTGGC  
 676 TGCAGGCTCGAGTTCAGGGGGCAGCTTTCCTGGCCCAGAGCCCAG  
  
 721 AGACCCCGGAGATGAGTGATGAGGACAGCTGTGTAGCCTGTGGAT  
     MetSerAspGluAspSerCysValAlaCysGlyS  
  
 766 CCTTGAGGACAGCAGGTCCCCAGGCAGGAGCACCTCCCCATGGC  
     erLeuArgThrAlaGlyProGlnAlaGlyAlaProSerProTrpP  
  
 811 CCTGGGAGGCCAGGCTGATGCACCAGGGACAGCTGGCCTGTGGCG  
     roTrpGluAlaArgLeuMetHisGlnGlyGlnLeuAlaCysGlyG  
  
 856 GAGCCCTGGTGTCTAGAGGAGGCGGTGCTAACTGCTGCCCACTGCT  
     lyAlaLeuValSerGluGluAlaValLeuThrAlaAlaHisCysP  
  
 901 TCAATGGGCGCCAGGCCCCAGAGGAATGGAGCGTAGGGCTGGGGA  
     heAsnGlyArgGlnAlaProGluGluTrpSerValGlyLeuGlyT  
  
 946 CCAGACCGGAGGAGTGGGGCCTGAAGCAGCTCATCCTGCATGGAG  
     hrArgProGluGluTrpGlyLeuLysGlnLeuIleLeuHisGlyA  
  
 991 CCTACACCCACCCTGAGGGGGGCTACGACATGGCCCTCCTGCTGC  
     laTyrThrHisProGluGlyGlyTyrAspMetAlaLeuLeuLeuL  
  
 1036 TGGCTCAGCCTGTGACACTGGGAGCCAGCCTGCGGGCCCTCTGCC  
     euAlaGlnProValThrLeuGlyAlaSerLeuArgAlaLeuCysL  
  
 1081 TGCCCTATTTTGACCACCACCTGCCTGATGGGGAGCGTGGCTGGG  
     euProTyrPheAspHisHisLeuProAspGlyGluArgGlyTrpV  
  
 1126 TTCTGGGACGGGCCCCGCCAGGAGCAGGCATCAGCTCCCTCCAGA  
     alLeuGlyArgAlaArgProGlyAlaGlyIleSerSerLeuGlnT  
  
 1171 CAGTGCCCGTGACCCTCCTGGGGCCTAGGGCCTGCAGCCGGCTGC  
     hrValProValThrLeuLeuGlyProArgAlaCysSerArgLeuH

Fig. 2

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1216 ATGCAGCTCCTGGGGGTGATGGCAGCCCTATTCTGCCGGGGATGG  
isAlaAlaProGlyGlyAspGlySerProIleLeuProGlyMetV

1261 TGTGTACCAGTGCTGTGGGTGAGCTGCCCAGCTGTGAGGGCCTGT  
alCysThrSerAlaValGlyGluLeuProSerCysGluGlyLeuS

1306 CTGGGGCACCACCTGGTGCATGAGGTGAGGGGCACATGGTTCCTGG  
erGlyAlaProLeuValHisGluValArgGlyThrTrpPheLeuA

1351 CCGGGCTGCACAGCTTCGGAGATGCTTGCCAAGGCCCGCCAGGC  
laGlyLeuHisSerPheGlyAspAlaCysGlnGlyProAlaArgP

1396 CGGCGGTCTTCACCGCGCTCCCTGCCTATGAGGACTGGGTCAGCA  
roAlaValPheThrAlaLeuProAlaTyrGluAspTrpValSerS

1441 GTTTGGACTGGCAGGTCTACTTCGCCGAGGAACCAGAGCCCGAGG  
erLeuAspTrpGlnValTyrPheAlaGluGluProGluProGluA

1486 CTGAGCCTGGAAGCTGCCTGGCCAACATAAGCCAACCAACCAGCT  
laGluProGlySerCysLeuAlaAsnIleSerGlnProThrSerC

1531 GCTGACAGGGGACCTGGCCATTCTCAGGACAAGAGAATGCAGGCA  
ys

1576 GGCAAATGGCATTACTGCCCCTGTCCTCCCCACCCTGTCATGTGT  
1621 GATTCCAGGCACCAGGGCAGGCCCAGAAGCCCAGCAGCTGTGGGA  
1666 AGGAACCTGCCTGGGGCCACAGGTGCCCCCTCCCCACCCTGCAGG  
1711 ACAGGGGTGTCTGTGGACACTCCCACACCCAACCTCTGCTACCAAG  
1756 CAGGCGTCTCAGCTTTCCTCCTCCTTTACCCTTTCAGATACAATC  
1801 ACGCCAGCCCCGTTGTTTTGAAAATTTCTTTTTTTGGGGGGCAGC  
1846 AGTTTTCTTTTTTTTAACTTAAATAAATTGTTACAAAATAGACT  
1891 TTAG

Fig. 2 (continued)

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1 GCGGATCCTCACACGACTGTGATCCGATTCTTTCCAGCGGCTTCT  
 46 GCAACCAAGCGGGTCTTACCCCCGGTCCTCCGCGTCTCCAGTCCT  
 91 CGCACCTGGAACCCCAACGTCCCCGAGAGTCCCCGAATCCCCGCT  
  
 136 CCCAGGCTACCTAAGAGGATGAGCGGTGCTCCGACGGCCGGGGCA  
                     MetSerGlyAlaProThrAlaGlyAla  
  
 181 GCCCTGATGCTCTGCGCCGCCACCGCCGTGCTACTGAGCGCTCAG  
                     AlaLeuMetLeuCysAlaAlaThrAlaValLeuLeuSerAlaGln  
  
 226 GGCGGACCCGTGCAGTCCAAGTCGCCGCGCTTTGCGTCCTGGGAC  
                     GlyGlyProValGlnSerLysSerProArgPheAlaSerTrpAsp  
  
 271 GAGATGAATGTCCTGGCGCACGGACTCCTGCAGCTCGGCCAGGGG  
                     GluMetAsnValLeuAlaHisGlyLeuLeuGlnLeuGlyGlnGly  
  
 316 TGCGCGAACACCGGAGCGCACCCGCAGTCAGCTGAGCGCGCTGGA  
                     CysAlaAsnThrGlyAlaHisProGlnSerAlaGluArgAlaGly  
  
 361 GCGCGCCTGAGCGCGTGCGGGTCCGCCTGTCAGGGAACCGAGGGG  
                     AlaArgLeuSerAlaCysGlySerAlaCysGlnGlyThrGluGly  
  
 406 TCCACCGACCTCCCGTTAGCCCCTGAGAGCCGGGTGGACCCTGAG  
                     SerThrAspLeuProLeuAlaProGluSerArgValAspProGlu  
  
 451 GTCCTTCACAGCCTGCAGACACAACCTCAAGGCTCAGAACAGCAGG  
                     ValLeuHisSerLeuGlnThrGlnLeuLysAlaGlnAsnSerArg  
  
 496 ATCCAGCAACTCTTCCACAAGGTGGCCCAGCAGCAGCGGCACCTG  
                     IleGlnGlnLeuPheHisLysValAlaGlnGlnGlnArgHisLeu  
  
 541 GAGAAGCAGCACCTGCGAATTCAGCATCTGCAAAGCCAGTTTGGC  
                     GluLysGlnHisLeuArgIleGlnHisLeuGlnSerGlnPheGly  
  
 586 CTCCTGGACCACAAGCACCTAGACCATGAGGTGGCCAAGCCTGCC  
                     LeuLeuAspHisLysHisLeuAspHisGluValAlaLysProAla  
  
 631 CGAAGAAAGAGGCTGCCCCGAGATGGCCCAGCCAGTTGACCCGGCT  
                     ArgArgLysArgLeuProGluMetAlaGlnProValAspProAla  
  
 676 CACAATGTCAGCCGCCTGCACCGGCTGCCCAGGGATTGCCAGGAG  
                     HisAsnValSerArgLeuHisArgLeuProArgAspCysGlnGlu  
  
 721 CTGTTCCAGGTTGGGGAGAGGCAGAGTGGACTATTTGAAATCCAG  
                     LeuPheGlnValGlyGluArgGlnSerGlyLeuPheGluIleGln  
  
 766 CCTCAGGGGTCTCCGCCATTTTTGGTGAAGTGAAGATGACCTCA  
                     ProGlnGlySerProProPheLeuValAsnCysLysMetThrSer

Fig. 3

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811 GATGGAGGCTGGACAGTAATTCAGAGGCGCCACGATGGCTCAGTG  
 AspGlyGlyTrpThrValIleGlnArgArgHisAspGlySerVal  
 856 GACTTCAACCGGCCCTGGGAAGCCTACAAGGCGGGGTTTGGGGAT  
 AspPheAsnArgProTrpGluAlaTyrLysAlaGlyPheGlyAsp  
 901 CCCCACGGCGAGTTCTGGCTGGGTCTGGAGAAGGTGCATAGCATG  
 ProHisGlyGluPheTrpLeuGlyLeuGluLysValHisSerMet  
 946 ATGGGGGACCGCAACAGCCGCCTGGCCGTGCAGCTGCGGGACTGG  
 MetGlyAspArgAsnSerArgLeuAlaValGlnLeuArgAspTrp  
 991 GATGGCAACGCCGAGTTGCTGCAGTTCTCCGTGCACCTGGGTGGC  
 AspGlyAsnAlaGluLeuLeuGlnPheSerValHisLeuGlyGly  
 1036 GAGGACACGGCCTATAGCCTGCAGCTCACTGCACCCGTGGCCGGC  
 GluAspThrAlaTyrSerLeuGlnLeuThrAlaProValAlaGly  
 1081 CAGCTGGGCGCCACCACCGTCCCACCCAGCGGCCTCTCCGTACCC  
 GlnLeuGlyAlaThrThrValProProSerGlyLeuSerValPro  
 1126 TTCTCCACTTGGGACCAGGATCACGACCTCCGCAGGGACAAGAAC  
 PheSerThrTrpAspGlnAspHisAspLeuArgArgAspLysAsn  
 1171 TGCGCCAAGAGCCTCTCTGGAGGCTGGTGGTTTGGCACCTGCAGC  
 CysAlaLysSerLeuSerGlyGlyTrpTrpPheGlyThrCysSer  
 1216 CATTCCAACCTCAACGGCCAGTACTTCCGCTCCATCCCACAGCAG  
 HisSerAsnLeuAsnGlyGlnTyrPheArgSerIleProGlnGln  
 1261 CGGCAGAAGCTTAAGAAGGGAATCTTCTGGAAGACCTGGCGGGGC  
 ArgGlnLysLeuLysLysGlyIlePheTrpLysThrTrpArgGly  
 1306 CGCTACTACCCGCTGCAGGCCACCACCATGTTGATCCAGCCCATG  
 ArgTyrTyrProLeuGlnAlaThrThrMetLeuIleGlnProMet  
 1351 GCAGCAGAGGCAGCCTCCTAGCGTCCTGGCTGGGCCTGGTCCCAG  
 AlaAlaGluAlaAlaSer  
 1396 GCCCACGAAAGACGGTGACTCTTGGCTCTGCCCCGAGGATGTGGCC  
 1441 GTTCCCTGCCTGGGCAGGGGCTCCAAGGAGGGGCCATCTGGAAAC  
 1486 TTGTGGACAGAGAAGAAGACCACGACTGGAGAAGCCCCCTTTCTG  
 1531 AGTGCAGGGGGGCTGCATGCGTTGCCTCCTGAGATCGAGGCTGCA  
 1576 GGATATGCTCAGACTCTAGAGGCGTGGACCAAGGGGCATGGAGCT  
 1621 TCACTCCTTGCTGGCCAGGGAGTTGGGGACTCAGAGGGACCACTT  
 1666 GGGGCCAGCCAGACTGGCCTCAATGGCGGACTCAGTCACATTGAC  
 1711 TGACGGGGACCAGGGCTTGTGTGGGTGCGAGAGCGCCCTCATGGTG  
 1756 CTGGTGCTGTTGTGTGTAGGTCCCCTGGGGACACAAGCAGGCGCC  
 1801 AATGGTATCTGGGCGGAGCTCACAGAGTTCTTGAATAAAAGCAA  
 1846 CCTCAGAACA

Fig. 3 (continued)

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1 GG TAGCCGACGCGCCGGCCGGCGCGTGACCTTGCCCCCTCTTGCTC  
 46 GCCTTGAAAATGGAAAAGATGCTCGCAGGCTGCTTTCTGCTGATC  
     MetGluLysMetLeuAlaGlyCysPheLeuLeuIle  
 91 CTCGGACAGATCGTCCTCCTCCCTGCCGAGGCCAGGGAGCGGTCA  
     LeuGlyGlnIleValLeuLeuProAlaGluAlaArgGluArgSer  
 136 CGTGGGAGGTCCATCTCTAGGGGCAGACACGCTCGGACCCACCCG  
     ArgGlyArgSerIleSerArgGlyArgHisAlaArgThrHisPro  
 181 CAGACGGCCCTTCTGGAGAGTTCCTGTGAGAACAAGCGGGCAGAC  
     GlnThrAlaLeuLeuGluSerSerCysGluAsnLysArgAlaAsp  
 226 CTGGTTTTTCATCATTGACAGCTCTCGCAGTGTCAACACCCATGAC  
     LeuValPheIleIleAspSerSerArgSerValAsnThrHisAsp  
 271 TATGCAAAGGTCAAGGAGTTCATCGTGGACATCTTGCAATTCTTG  
     TyrAlaLysValLysGluPheIleValAspIleLeuGlnPheLeu  
 316 GACATTGGTCCTGATGTCACCCGAGTGGGCCTGCTCCAATATGGC  
     AspIleGlyProAspValThrArgValGlyLeuLeuGlnTyrGly  
 361 AGCACTGTCAAGAATGAGTTCCTCCCTCAAGACCTTCAAGAGGAAG  
     SerThrValLysAsnGluPheSerLeuLysThrPheLysArgLys  
 406 TCCGAGGTGGAGCGTGCTGTCAAGAGGATGCGGCATCTGTCCACG  
     SerGluValGluArgAlaValLysArgMetArgHisLeuSerThr  
 451 GGCACCATGACTGGGCTGGCCATCCAGTATGCCCTGAACATCGCA  
     GlyThrMetThrGlyLeuAlaIleGlnTyrAlaLeuAsnIleAla  
 496 TTCTCAGAAGCAGAGGGGGCCCGGCCCTGAGGGAGAATGTGCCA  
     PheSerGluAlaGluGlyAlaArgProLeuArgGluAsnValPro  
 541 CGGGTCATAATGATCGTGACGGATGGGAGACCTCAGGACTCCGTG  
     ArgValIleMetIleValThrAspGlyArgProGlnAspSerVal  
 586 GCCGAGGTGGCTGCTAAGGCACGGGACACGGGCATCCTAATCTTT  
     AlaGluValAlaAlaLysAlaArgAspThrGlyIleLeuIlePhe  
 631 GCCATTGGTGTGGGCCAGGTAGACTTCAACACCTTGAAGTCCATT  
     AlaIleGlyValGlyGlnValAspPheAsnThrLeuLysSerIle  
 676 GGGAGTGAGCCCCATGAGGACCATGTCTTCCTTGTGGCCAATTTT  
     GlySerGluProHisGluAspHisValPheLeuValAlaAsnPhe  
 721 AGCCAGATTGAGACGCTGACCTCCGTGTTCCAGAAGAAGTTGTGC  
     SerGlnIleGluThrLeuThrSerValPheGlnLysLysLeuCys

Fig. 4

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766 ACGGCCACATGTGCAGCACCTGGAGCATAACTGTGCCCACTTC  
 ThrAlaHisMetCysSerThrLeuGluHisAsnCysAlaHisPhe  
 811 TGCATCAACATCCCTGGCTCATACGTCTGCAGGTGCAAACAAGGC  
 CysIleAsnIleProGlySerTyrValCysArgCysLysGlnGly  
 856 TACATTCTCAACTCGGATCAGACGACTTGCAGAATCCAGGATCTG  
 TyrIleLeuAsnSerAspGlnThrThrCysArgIleGlnAspLeu  
 901 TGTGCCATGGAGGACCACAACCTGTGAGCAGCTCTGTGTGAATGTG  
 CysAlaMetGluAspHisAsnCysGluGlnLeuCysValAsnVal  
 946 CCGGGCTCCTTCGTCTGCGAGTGCTACAGTGGCTACGCCCTGGCT  
 ProGlySerPheValCysGluCysTyrSerGlyTyrAlaLeuAla  
 991 GAGGATGGGAAGAGGTGTGTGGCTGTGGACTACTGTGCCTCAGAA  
 GluAspGlyLysArgCysValAlaValAspTyrCysAlaSerGlu  
 1036 AACCACGGATGTGAACATGAGTGTGTAAATGCTGATGGCTCCTAC  
 AsnHisGlyCysGluHisGluCysValAsnAlaAspGlySerTyr  
 1081 CTTTGCCAGTGCCATGAAGGATTTGCTCTTAACCCAGATGAAAAA  
 LeuCysGlnCysHisGluGlyPheAlaLeuAsnProAspGluLys  
 1126 ACGTGCACAAAGATAGACTACTGTGCCTCATCTAATCATGGATGT  
 ThrCysThrLysIleAspTyrCysAlaSerSerAsnHisGlyCys  
 1171 CAGTACGAGTGTGTTAACACAGATGATTCCTATTCTGCCACTGC  
 GlnTyrGluCysValAsnThrAspAspSerTyrSerCysHisCys  
 1216 CTGAAAGGCTTTACCCTGAATCCAGATAAGAAAACCTGCAGAAGG  
 LeuLysGlyPheThrLeuAsnProAspLysLysThrCysArgArg  
 1261 ATCAACTACTGTGCACTGAACAAACCGGGCTGTGAGCATGAGTGC  
 IleAsnTyrCysAlaLeuAsnLysProGlyCysGluHisGluCys  
 1306 GTCAACATGGAGGAGAGCTACTACTGCCGCTGCCACCGTGGCTAC  
 ValAsnMetGluGluSerTyrTyrCysArgCysHisArgGlyTyr  
 1351 ACTCTGGACCCCAATGGCAAACCTGCAGCCGAGTGGACCACTGT  
 ThrLeuAspProAsnGlyLysProCysSerArgValAspHisCys  
 1396 GCACAGCAGGACCATGGCTGTGAGCAGCTGTGTCTGAACACGGAG  
 AlaGlnGlnAspHisGlyCysGluGlnLeuCysLeuAsnThrGlu  
 1441 GATTCCTTCGTCTGCCAGTGCTCAGAAGGCTTCCTCATCAACGAG  
 AspSerPheValCysGlnCysSerGluGlyPheLeuIleAsnGlu

Fig. 4 (continued)

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1486 GACCTCAAGACCTGCTCCCGGGTGGATTACTGCCTGCTGAGTGAC  
 AspLeuLysThrCysSerArgValAspTyrCysLeuLeuSerAsp  
 1531 CATGGTTGTGAATACTCCTGTGTCAACATGGACAGATCCTTTGCC  
 HisGlyCysGluTyrSerCysValAsnMetAspArgSerPheAla  
 1576 TGTCAGTGTCTGAGGGACACGTGCTCCGCAGCGATGGGAAGACG  
 CysGlnCysProGluGlyHisValLeuArgSerAspGlyLysThr  
 1621 TGTGCAAAATTGGACTCTTGTGCTCTGGGGGACCACGGTTGTGAA  
 CysAlaLysLeuAspSerCysAlaLeuGlyAspHisGlyCysGlu  
 1666 CATTCTGTGTGAAGCAGTGAAGATTCGTTTGTGTGCCAGTGCTTT  
 HisSerCysValSerSerGluAspSerPheValCysGlnCysPhe  
 1711 GAAGGTTATATACTCCGTGAAGATGGAAAAACCTGCAGAAGGAAA  
 GluGlyTyrIleLeuArgGluAspGlyLysThrCysArgArgLys  
 1756 GATGTCTGCCAAGCTATAGACCATGGCTGTGAACACATTTGTGTG  
 AspValCysGlnAlaIleAspHisGlyCysGluHisIleCysVal  
 1801 AACAGTGACGACTCATACACGTGCGAGTGCTTGGAGGGATTCCGG  
 AsnSerAspAspSerTyrThrCysGluCysLeuGluGlyPheArg  
 1846 CTCACTGAGGATGGGAAACGCTGCCGAATTCCTCAGGGAAGGAT  
 LeuThrGluAspGlyLysArgCysArgIleSerSerGlyLysAsp  
 1891 GTCTGCAAATCAACCCACCATGGCTGCGAACACATTTGTGTTAAT  
 ValCysLysSerThrHisHisGlyCysGluHisIleCysValAsn  
 1936 AATGGGAATTCCTACATCTGCAAATGCTCAGAGGGATTTGTTCTA  
 AsnGlyAsnSerTyrIleCysLysCysSerGluGlyPheValLeu  
 1981 GCTGAGGACGGAAGACGGTGCAAGAAATGCACTGAAGGCCCAATT  
 AlaGluAspGlyArgArgCysLysLysCysThrGluGlyProIle  
 2026 GACCTGGTCTTTGTGATCGATGGATCCAAGAGTCTTGGAGAAGAG  
 AspLeuValPheValIleAspGlySerLysSerLeuGlyGluGlu  
 2071 AATTTTGAGGTCGTGAAGCAGTTTGTCACTGGAATTATAGATTCC  
 AsnPheGluValValLysGlnPheValThrGlyIleIleAspSer  
 2116 TTGACAATTTCCCCCAAAGCCGCTCGAGTGGGGCTGCTCCAGTAT  
 LeuThrIleSerProLysAlaAlaArgValGlyLeuLeuGlnTyr  
 2161 TCCACACAGGTCCACACAGAGTTCACTCTGAGAACTTCAACTCA  
 SerThrGlnValHisThrGluPheThrLeuArgAsnPheAsnSer  
 2206 GCCAAAGACATGAAAAAAGCCGTGGCCACATGAAATACATGGGA  
 AlaLysAspMetLysLysAlaValAlaHisMetLysTyrMetGly

Fig. 4 (continued)

2251 AAGGGCTCTATGACTGGGCTGGCCCTGAAACACATGTTTGAGAGA  
LysGlySerMetThrGlyLeuAlaLeuLysHisMetPheGluArg

2296 AGTTTTACCCAAGGAGAAGGGGCCAGGCCCTTTTCCACAAGGGT  
SerPheThrGlnGlyGluGlyAlaArgProLeuPheHisLysGly

2341 GCCCAGAGCAGCCATTGTGTTTACCGACGGACGGGCTCAGGATGA  
AlaGlnSerSerHisCysValHisArgArgThrGlySerGly

2386 CGTCTCCGAGTGGGCCAGTAAAGCCAAGGCCAATGGTATCACTAT  
2431 GTATGCTGTTGGGGTAGGAAAAGCCATTGAGGAGGAACCTACAAGA  
2476 GATTGCCTCTGAGCCCACAAACAAGCATCTCTTCTATGCCGAAGA  
2521 CTTCAGCACAAATGGATGAGATAAGTGAAAAACTCAAGAAAGGCAT  
2566 CTGTGAAGCTCTAGAAGACTCCGATGGAAGACAGGACTCTCCAGC  
2611 AGGGGAAC TGCCAAAAACGGTCCAACAGCCAACAGAATCTGAGCC  
2656 AGTCACCATAAATATCCAAGACCTACTTTCCTGTTCTAATTTTGC  
2701 AGTGCAACACAGATATCTGTTTGAAGAAGACAATCTTTTACGGTC  
2746 TACACAAAAGCTTTCCCATTCAACAAAACCTTCAGGAAGCCCTTT  
2791 GGAAGAAAAACACGATCAATGCAAATGTGAAAACCTTATAATGTT  
2836 CCAGAACCTTGCAAACGAAGAAGTAAGAAAATTTACACAGCGCTT  
2881 AGAAGAAATGACACAGAGAATGGAAGCCCTGGAAAATCGCCTGAG  
2926 ATACAGATGAAGATTAGAAATCGCGACACATTTGTAGTCATTGTA  
2971 TCACGGATTACAATGAACGCAGTGCAGAGCCCCAAAGCTCAGGCT  
3016 ATTGTTAAATC

Fig. 4 (continued)



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1 GGTAGCCGACGCGCCGGCCGGCGCGTGACCTTGCCCCTCTTGCTC  
 46 GCCTTGAAAATGGAAAAGATGCTCGCAGGCTGCTTTCTGCTGATC  
 MetGluLysMetLeuAlaGlyCysPheLeuLeuIle  
 91 CTCGGACAGATCGTCCTCCTCCCCTGCGAGGCCAGGGAGCGGTCA  
 LeuGlyGlnIleValLeuLeuProCysGluAlaArgGluArgSer  
 136 CGTGGGAGGTCCATCTCTAGGGGCAGACACGCTCGGACCCACCCG  
 ArgGlyArgSerIleSerArgGlyArgHisAlaArgThrHisPro  
 181 CAGACGGCCCTTCTGGAGAGTTCCTGTGAGAACAAGCGGGCAGAC  
 GlnThrAlaLeuLeuGluSerSerCysGluAsnLysArgAlaAsp  
 226 CTGGTTTTTCATCATTGACAGCTCTCGCAGTGTCAACACCCATGAC  
 LeuValPheIleIleAspSerSerArgSerValAsnThrHisAsp  
 271 TATGCAAAGGTCAAGGAGTTCATCGTGACATCTTGCAATTCTTG  
 TyrAlaLysValLysGluPheIleValAspIleLeuGlnPheLeu  
 316 GACATTGGTCCTGATGTCACCCGAGTGGGCCTGCTCCAATATGGC  
 AspIleGlyProAspValThrArgValGlyLeuLeuGlnTyrGly  
 361 AGCACTGTCAAGAATGAGTTCTCCCTCAAGACCTTCAAGAGGAAG  
 SerThrValLysAsnGluPheSerLeuLysThrPheLysArgLys  
 406 TCCGAGGTGGAGCGTGCTGTCAAGAGGATGCGGCATCTGTCCACG  
 SerGluValGluArgAlaValLysArgMetArgHisLeuSerThr  
 451 GGCACCATGACTGGGCTGGCCATCCAGTATGCCCTGAACATCGCA  
 GlyThrMetThrGlyLeuAlaIleGlnTyrAlaLeuAsnIleAla  
 496 TTCTCAGAAGCAGAGGGGGCCCGCCCCCTGAGGGAGAATGTGCCA  
 PheSerGluAlaGluGlyAlaArgProLeuArgGluAsnValPro  
 541 CGGGTCATAATGATCGTGACGGATGGGAGACCTCAGGACTCCGTG  
 ArgValIleMetIleValThrAspGlyArgProGlnAspSerVal  
 586 GCCGAGGTGGCTGCTAAGGCACGGGACACGGGCATCCTAATCTTT  
 AlaGluValAlaAlaLysAlaArgAspThrGlyIleLeuIlePhe  
 631 GCCATTGGTGTGGGCCAGGTAGACTTCAACACCTTGAAGTCCATT  
 AlaIleGlyValGlyGlnValAspPheAsnThrLeuLysSerIle  
 676 GGGAGTGAGCCCCATGAGGACCATGTCTTCCTTGTGGCCAATTTT  
 GlySerGluProHisGluAspHisValPheLeuValAlaAsnPhe  
 721 AGCCAGATTGAGACGCTGACCTCCGTGTTCCAGAAGAAGTTGTGC  
 SerGlnIleGluThrLeuThrSerValPheGlnLysLysLeuCys

Fig. 5

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766 ACGGCCACATGTGCAGCACCCCTGGAGCATAACTGTGCCCACTTC  
 ThrAlaHisMetCysSerThrLeuGluHisAsnCysAlaHisPhe  
 811 TGCATCAACATCCCTGGCTCATACGTCTGCAGGTGCAAACAAGGC  
 CysIleAsnIleProGlySerTyrValCysArgCysLysGlnGly  
 856 TACATTCTCAACTCGGATCAGACGACTTGCAGAATCCAGGATCTG  
 TyrIleLeuAsnSerAspGlnThrThrCysArgIleGlnAspLeu  
 901 TGTGCCATGGAGGACCACAACCTGTGAGCAGCTCTGTGTGAATGTG  
 CysAlaMetGluAspHisAsnCysGluGlnLeuCysValAsnVal  
 946 CCGGGCTCCTTCGTCTGCGAGTGCTACAGTGGCTACGCCCTGGCT  
 ProGlySerPheValCysGluCysTyrSerGlyTyrAlaLeuAla  
 991 GAGGATGGGAAGAGGTGTGTGGCTGTGGACTACTGTGCCTCAGAA  
 GluAspGlyLysArgCysValAlaValAspTyrCysAlaSerGlu  
 1036 AACCACGGATGTGAACATGAGTGTGTAAATGCTGATGGCTCCTAC  
 AsnHisGlyCysGluHisGluCysValAsnAlaAspGlySerTyr  
 1081 CTTTGCCAGTGCCATGAAGGATTTGCTCTTAACCCAGATGAAAAA  
 LeuCysGlnCysHisGluGlyPheAlaLeuAsnProAspGluLys  
 1126 ACGTGCACAAAGATAGACTACTGTGCCTCATCTAATCATGGATGT  
 ThrCysThrLysIleAspTyrCysAlaSerSerAsnHisGlyCys  
 1171 CAGTACGAGTGTGTTAACACAGATGATTCCTATTCCTGCCACTGC  
 GlnTyrGluCysValAsnThrAspAspSerTyrSerCysHisCys  
 1216 CTGAAAGGCTTTACCCTGAATCCAGATAAGAAAACCTGCAGAAGG  
 LeuLysGlyPheThrLeuAsnProAspLysLysThrCysArgArg  
 1261 ATCAACTACTGTGCACTGAACAAACCGGGCTGTGAGCATGAGTGC  
 IleAsnTyrCysAlaLeuAsnLysProGlyCysGluHisGluCys  
 1306 GTCAACATGGAGGAGAGCTACTACTGCCGCTGCCACCGTGGCTAC  
 ValAsnMetGluGluSerTyrTyrCysArgCysHisArgGlyTyr  
 1351 ACTCTGGACCCCAATGGCAAACCCTGCAGCCGAGTGGACCACTGT  
 ThrLeuAspProAsnGlyLysProCysSerArgValAspHisCys  
 1396 GCACAGCAGGACCATGGCTGTGAGCAGCTGTGTCTGAACACGGAG  
 AlaGlnGlnAspHisGlyCysGluGlnLeuCysLeuAsnThrGlu  
 1441 GATTCCTTCGTCTGCCAGTGCTCAGAAGGCTTCCTCATCAACGAG  
 AspSerPheValCysGlnCysSerGluGlyPheLeuIleAsnGlu  
 1486 GACCTCAAGACCTGCTCCCGGGTGGATTACTGCCTGCTGAGTGAC  
 AspLeuLysThrCysSerArgValAspTyrCysLeuLeuSerAsp

Fig. 5 (continued)

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1531 CATGGTTGTGAATACTCCTGTGTCAACATGGACAGATCCTTTGCC  
HisGlyCysGluTyrSerCysValAsnMetAspArgSerPheAla

1576 TGTCAGTGTCTTGAGGGACACGTGCTCCGCAGCGATGGGAAGACG  
CysGlnCysProGluGlyHisValLeuArgSerAspGlyLysThr

1621 TGTGCAAAATTGGACTCTTGTGCTCTGGGGGACCACGGTTGTGAA  
CysAlaLysLeuAspSerCysAlaLeuGlyAspHisGlyCysGlu

1666 CATTCGTGTGTAAGCAGTGAAGATTCGTTTGTGTGCCAGTGCTTT  
HisSerCysValSerSerGluAspSerPheValCysGlnCysPhe

1711 GAAGGTTATATACTCCGTGAAGATGGAAAAACCTGCAGAAGGAAA  
GluGlyTyrIleLeuArgGluAspGlyLysThrCysArgArgLys

1756 GATGTCTGCCAAGCTATAGACCATGGCTGTGAACACATTTGTGTG  
AspValCysGlnAlaIleAspHisGlyCysGluHisIleCysVal

1801 AACAGTGACGACTCATACACGTGCGAGTGCTTGGAGGGATTCCGG  
AsnSerAspAspSerTyrThrCysGluCysLeuGluGlyPheArg

1846 CTCACTGAGGATGGGAAACGCTGCCGAATTCCTCAGGGAAGGAT  
LeuThrGluAspGlyLysArgCysArgIleSerSerGlyLysAsp

1891 GTCTGCAAATCAACCCACCATGGCTGCGAACACATTTGTGTTAAT  
ValCysLysSerThrHisHisGlyCysGluHisIleCysValAsn

1936 AATGGGAATTCCTACATCTGCAAATGCTCAGAGGGATTTGTTCTA  
AsnGlyAsnSerTyrIleCysLysCysSerGluGlyPheValLeu

1981 GCTGAGGACGGAAGACGGTGCAAGAAATGCACTGAAGGCCCAATT  
AlaGluAspGlyArgArgCysLysLysCysThrGluGlyProIle

2026 GACCTGGTCTTTGTGATCGATGGATCCAAGAGTCTTGGAGAAGAG  
AspLeuValPheValIleAspGlySerLysSerLeuGlyGluGlu

2071 AATTTTGAGGTCGTGAAGCAGTTTGTCACTGGAATTATAGATTCC  
AsnPheGluValValLysGlnPheValThrGlyIleIleAspSer

2116 TTGACAATTTCCCCCAAAGCCGCTCGAGTGGGGCTGCTCCAGTAT  
LeuThrIleSerProLysAlaAlaArgValGlyLeuLeuGlnTyr

2161 TCCACACAGGTCCACACAGAGTTCACTCTGAGAACTTCAACTCA  
SerThrGlnValHisThrGluPheThrLeuArgAsnPheAsnSer

2206 GCCAAAGACATGAAAAAAGCCGTGGCCCACATGAAATACATGGGA  
AlaLysAspMetLysLysAlaValAlaHisMetLysTyrMetGly

Fig. 5 (continued)

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2251 AAGGGCTCTATGACTGGGCTGGCCCTGAAACACATGTTTGAGAGA  
LysGlySerMetThrGlyLeuAlaLeuLysHisMetPheGluArg

2296 AGTTTTACCCAAGGAGAAGGGGCCAGGCCCTTTTCCACAAGGGTG  
SerPheThrGlnGlyGluGlyAlaArgProPheSerThrArgVal

2341 CCCAGAGCAGCCATTGTGTTCACCGACGGACGGGCTCAGGATGAC  
ProArgAlaAlaIleValPheThrAspGlyArgAlaGlnAspAsp

2386 GTCTCCGAGTGGGCCAGTAAAGCCAAGGCCAATGGTATCACTATG  
ValSerGluTrpAlaSerLysAlaLysAlaAsnGlyIleThrMet

2431 TATGCTGTTGGGGTAGGAAAAGCCATTGAGGAGGAAC TACAAGAG  
TyrAlaValGlyValGlyLysAlaIleGluGluGluLeuGlnGlu

2476 ATTGCCTCTGAGCCCACAAACAAGCATCTCTTCTATGCCGAAGAC  
IleAlaSerGluProThrAsnLysHisLeuPheTyrAlaGluAsp

2521 TTCAGCACAATGGATGAGATAAGTGAAAAACTCAAGAAAGGCATC  
PheSerThrMetAspGluIleSerGluLysLeuLysLysGlyIle

2566 TGTGAAGCTCTAGAAGACTCCGATGGAAGACAGGACTCTCCAGCA  
CysGluAlaLeuGluAspSerAspGlyArgGlnAspSerProAla

2611 GGGGAACTGCCAAAAACGGTCCAACAGCCAACAGAATCTGAGCCA  
GlyGluLeuProLysThrValGlnGlnProThrGluSerGluPro

2656 GTCACCATAAATATCCAAGACCTACTTTCCTGTTCTAATTTTGCA  
ValThrIleAsnIleGlnAspLeuLeuSerCysSerAsnPheAla

2701 GTGCAACACAGATATCTGTTTGAAGAAGACAATCTTTTACGGTCT  
ValGlnHisArgTyrLeuPheGluGluAspAsnLeuLeuArgSer

2746 ACACAAAAGCTTTCCCATTTCAACAAAACCTTCAGGAAGCCCTTTG  
ThrGlnLysLeuSerHisSerThrLysProSerGlySerProLeu

2791 GAAGAAAAACACGATCAATGCAAATGTGAAAACCTTATAATGTTC  
GluGluLysHisAspGlnCysLysCysGluAsnLeuIleMetPhe

2836 CAGAACCTTGCAAACGAAGAAGTAAGAAAATTAACACAGCGCTTA  
GlnAsnLeuAlaAsnGluGluValArgLysLeuThrGlnArgLeu

2881 GAAGAAATGACACAGAGAATGGAAGCCCTGGAAAATCGCCTGAGA  
GluGluMetThrGlnArgMetGluAlaLeuGluAsnArgLeuArg

2926 TACAGATGAAGATTAGAAATCGCGACACATTTGTAGTCATTGTAT  
TyrArg

Fig. 5 (continued)

2971 CACGGATTACAATGAACGCAGTGCAGAGCCCCAAAGCTCAGGCTA  
3016 TTGTTAAATCAATAATGTTGTGAAGTAAAACAATCAGTACTGAGA  
3061 AACCTGGTTTGCCACAGAACAAAGACAAGAAGTATACACTAACTT  
3106 GTATAAATTTATCTAGGAAAAAAATCCTTCAGAATTCTAAGATGA  
3151 ATTTACCAGGTGAGAATGAATAAGCTATGCAAGGTATTTTGTAAT  
3196 ATACTGTGGACACAACCTTGCTTCTGCCTCATCCTGCCTTAGTGTG  
3241 CAATCTCATTTGACTATACGATAAAGTTTGCACAGTCTTACTTCT  
3286 GTAGAACACTGGCCATAGGAAATGCTGTTTTTTTGTACTGGACTT  
3331 TACCTTGATATATGTATATGGATGTATGCATAAAATCATAGGACA  
3376 TATGTACTTGTGGAACAAGTTGGATTTTTTTATACAATATTAAAT  
3421 TCACCACCTTCAGAGAAAAGTAAAAAAA

Fig. 5 (continued)

1 CGGCCCTTCTCACACTCCTGCCCTGCTGATGTGGAACGGGGTTTG  
46 GGGTTCTGCAGGGCTATTGTCTGCGCTGGGGAAGGGGACAGGCCG  
91 GGACCGGGACCTCCGCTCGCAGCCGGCCGCACCAGCAGGACAGCT

136 GGCCTGAAGCTCAGAGCCGGGGCGTGCGCCATGGCCCCACACTGG  
MetAlaProHisTrp

181 GCTGTCTGGCTGCTGGCAGCAAGGCTGTGGGGCCTGGGCATTGGG  
AlaValTrpLeuLeuAlaAlaArgLeuTrpGlyLeuGlyIleGly

226 GCTGAGGTGTGGTGGAACTTGTGCCGCGTAAGACAGTGTCTTCT  
AlaGluValTrpTrpAsnLeuValProArgLysThrValSerSer

271 GGGGAGCTGGCCACGGTAGTACGGCGGTCTCCAGACCGGCATC  
GlyGluLeuAlaThrValValArgArgPheSerGlnThrGlyIle

316 CAGGACTTCCTGACACTGACGCTGACGGAGCCCACTGGGCTTCTG  
GlnAspPheLeuThrLeuThrLeuThrGluProThrGlyLeuLeu

361 TACGTGGGCGCCCGAGAGGCCCTGTTTGCCTTCAGCATGGAGGCC  
TyrValGlyAlaArgGluAlaLeuPheAlaPheSerMetGluAla

406 CTGGAGCTGCAAGGAGCGATCTCCTGGGAGGCCCGTGGAGAAG  
LeuGluLeuGlnGlyAlaIleSerTrpGluAlaProValGluLys

451 AAGACTGAGTGTATCCAGAAAGGGAAGAACAACCAGACCGAGTGC  
LysThrGluCysIleGlnLysGlyLysAsnAsnGlnThrGluCys

496 TTCAACTTCATCCGCTTCCTGCAGCCCTACAATGCCTCCCACCTG  
PheAsnPheIleArgPheLeuGlnProTyrAsnAlaSerHisLeu

541 TACGTCTGTGGCACCTACGCCTTCCAGCCCAAGTGCACCTACGTC  
TyrValCysGlyThrTyrAlaPheGlnProLysCysThrTyrVal

586 AACATGCTCACCTTCACTTTGGAGCATGGAGAGTTTGAAGATGGG  
AsnMetLeuThrPheThrLeuGluHisGlyGluPheGluAspGly

631 AAGGGCAAGTGTCCCTATGACCCAGCTAAGGGCCATGCTGGCCTT  
LysGlyLysCysProTyrAspProAlaLysGlyHisAlaGlyLeu

676 CTTGTGGATGGTGAGCTGTACTCGGCCACACTCAACAACCTCCTG  
LeuValAspGlyGluLeuTyrSerAlaThrLeuAsnAsnPheLeu

721 GGCACGGAACCCATTATCCTGCGTAACATGGGGCCCCACCACTCC  
GlyThrGluProIleIleLeuArgAsnMetGlyProHisHisSer

Fig. 6

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766 ATGAAGACAGAGTACCTGGCCTTTTGGCTCAACGAACCTCACTTT  
MetLysThrGluTyrLeuAlaPheTrpLeuAsnGluProHisPhe

811 GTAGGCTCTGCCTATGTACCTGAGAGGGTGGGCCTGCTGTGGACA  
ValGlySerAlaTyrValProGluArgValGlyLeuLeuTrpThr

856 ATGGCATACTCTCTTCCAGCCCTAGGAGGAGGGCTCCTAACAGTG  
MetAlaTyrSerLeuProAlaLeuGlyGlyGlyLeuLeuThrVal

901 TAACTTATTGTGTCCCCGCGTATTTATTTGTTGTAAATATTTGAG  
946 TATTTTTTATATTGACAAATAAA

Fig. 6 (continued)

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1 GGCACCAGGCCTTCCGGAGAGACGCAGTCGGCTGCCACCCCGGGA  
 M  
 46 TGGGTCGCTGGTGCCAGACCGTCGCGCGCGGGCAGCGCCCCCGGA  
 etGlyArgTrpCysGlnThrValAlaArgGlyGlnArgProArgT  
 91 CGTCTGCCCCCTCCCGCGCCGGTGCCCTGCTGCTGCTGCTTCTGT  
 hrSerAlaProSerArgAlaGlyAlaLeuLeuLeuLeuLeuL  
 136 TGCTGAGGTCTGCAGGTTGCTGGGGCGCAGGGGAAGCCCCGGGGG  
 euLeuArgSerAlaGlyCysTrpGlyAlaGlyGluAlaProGlyA  
 181 CGCTGTCCACTGCTGATCCCGCCGACCAGAGCGTCCAGTGTGTCC  
 laLeuSerThrAlaAspProAlaAspGlnSerValGlnCysValP  
 226 CCAAGGCCACCTGTCCTTCCAGCCGGCCTCGCCTTCTCTGGCAGA  
 roLysAlaThrCysProSerSerArgProArgLeuLeuTrpGlnT  
 271 CCCCGACCACCCAGACACTGCCCTCGACCACCATGGAGACCCAAT  
 hrProThrThrGlnThrLeuProSerThrThrMetGluThrGlnP  
 316 TCCCAGTTTCTGAAGGCAAAGTCGACCCATACCGCTCCTGTGGCT  
 heProValSerGluGlyLysValAspProTyrArgSerCysGlyP  
 361 TTTCCTACGAGCAGGACCCACCCCTCAGGGACCCAGAAGCCGTGG  
 heSerTyrGluGlnAspProThrLeuArgAspProGluAlaValA  
 406 CTCGGCGGTGGCCCTGGATGGTCAGCGTGCGGGCCAATGGCACAC  
 laArgArgTrpProTrpMetValSerValArgAlaAsnGlyThrH  
 451 ACATCTGTGCCGGCACCATCATTGCCTCCCAGTGGGTGCTGACTG  
 isIleCysAlaGlyThrIleIleAlaSerGlnTrpValLeuThrV  
 496 TGGCCCACTGCCTGATCTGGCGTGATGTTATCTACTCAGTGAGGG  
 alAlaHisCysLeuIleTrpArgAspValIleTyrSerValArgV  
 541 TGGGGAGTCCGTGGATTGACCAGATGACGCAGACCGCCTCCGATG  
 alGlySerProTrpIleAspGlnMetThrGlnThrAlaSerAspV  
 586 TCCCGGTGCTCCAGGTCATCATGCATAGCAGGTACCGGGCCCAGC  
 alProValLeuGlnValIleMetHisSerArgTyrArgAlaGlnA  
 631 GGTTCTGGTCCTGGGTGGGCCAGGCCAACGACATCGGCCTCCTCA  
 rgPheTrpSerTrpValGlyGlnAlaAsnAspIleGlyLeuLeuL  
 676 AGCTCAAGCAGGAACCTCAAGTACAGCAATTACGTGCGGGCCCATCT  
 ysLeuLysGlnGluLeuLysTyrSerAsnTyrValArgProIleC

Fig. 7



721 GCCTGCCTGGCACGGACTATGTGTTGAAGGACCATTCCTCGCTGCA  
 ysLeuProGlyThrAspTyrValLeuLysAspHisSerArgCysT  
 766 CTGTGACGGGCTGGGGACTTTCCAAGGCTGACGGCATGTGGCCTC  
 hrValThrGlyTrpGlyLeuSerLysAlaAspGlyMetTrpProG  
 811 AGTTCCGGACCATTTCAGGAGAAGGAAGTCATCATCCTGAACAACA  
 lnPheArgThrIleGlnGluLysGluValIleIleLeuAsnAsnL  
 856 AAGAGTGTGACAATTTCTACCACAACCTTCACCAAATCCCCACTC  
 ysGluCysAspAsnPheTyrHisAsnPheThrLysIleProThrL  
 901 TGGTTCAGATCATCAAGTCCCAGATGATGTGTGCGGAGGACACCC  
 euValGlnIleIleLysSerGlnMetMetCysAlaGluAspThrH  
 946 ACAGGGAGAAGTTCTGCTATGAGCTAACTGGAGAGCCCTTGGTCT  
 isArgGluLysPheCysTyrGluLeuThrGlyGluProLeuValC  
 991 GCTCCATGGAGGGCACGTGGTACCTGGTGGGATTGGTGAGCTGGG  
 ysSerMetGluGlyThrTrpTyrLeuValGlyLeuValSerTrpG  
 1036 GTGCAGGCTGCCAGAAGAGCGAGGCCCCACCCATCTACCTACAGG  
 lyAlaGlyCysGlnLysSerGluAlaProProIleTyrLeuGlnV  
 1081 TCTCCTCCTACCAACACTGGATCTGGGACTGCCTCAACGGGCAGG  
 alSerSerTyrGlnHisTrpIleTrpAspCysLeuAsnGlyGlnA  
 1126 CCCTGGCCCTGCCAGCCCCATCCAGGACCCTGCTCCTGGCACTCC  
 laLeuAlaLeuProAlaProSerArgThrLeuLeuLeuAlaLeuP  
 1171 CACTGCCCCCTCAGCCTCCTTGCTGCCCTCTGACTCTGTGTGCCCT  
 roLeuProLeuSerLeuLeuAlaAlaLeu  
 1216 CCCTCACTTGTGGGCCCCCCTTGCTCCGTGCCCAGGTTGCTGTG  
 1261 GGTGCAGCTGTCACAGCCCTGAGAGTCAGGGTGGAGATGAGGTGC  
 1306 TCAATTAAACATTACTGTTTTCCATGTAAAAAAAAAAAAAAAAAAAA  
 1351 AAAAAAAAAA

Fig. 7 (continued)

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CACCCCTCTGCCTGCCCCAGCCCGCCCATCGCTTCCCCTTTGGAGCCTCCTGCTGGGCCACTGGCTGGGATCAGGACACC  
 81  
 AGTGATGGTAAGTGCTGGCCCAGACTGAAGCTCGGAGAGGCACTCTGCTTGCCCAGCGTCACAGTCTTAGCTCCCAACTG  
 161  
 TCCTGGCTTCCAGTCTCCCCTTGCTTCCCAGATCCCAGACTCTAGCCCCAGCCCCGTCTCTTTCACCAGCTCCTGGGACCC  
 241  
 TACGCAATCTGCGCCTGCGTCTCATCAGTCGCCCCACATGTAACGTATCTACAACCAGCTGCACCAGCGACACCTGTCC  
 321  
 AACCCGGCCCCGGCTGGGATGCTATGTGGGGGCCCCAGCCTGGGGTGCAGGGCCCCGTGCAGGTCTGATAGGGAGAAGA  
 401  
 GAAGGAGCAGAAGGGGAGGGGCCTAACCTGGGCTGGGGTGGACTCACAGGACTGGGGGAAAGAGCTGCAATCAGAGG  
 481  
 GTGTCTGCCATAGCTGGGCTCAGGCATCTGTCTTGGCTTTGTTGCCTGGCTCCAGGGAGATTCCGGGGGCCCTGTGCTG  
 561  
 TGCCTCGAGCCTGACGGACACTGGGTTTCAAGCTGGCATCATCAGCTTTGCATCAAGCTGTGCCCAGGAGGACGCTCCTGT  
 641  
 GCTGCTGACCAACACAGCTGCTCACAGTTCTGGCTGCAGGCTCGAGTTCAGGGGGCAGCTTTCCTGGCCCAGAGCCCAG  
 721  
 AGACCCCGGAGATGAGTGATGAGGACAGCTGTGTAGCCTGTGGATCCTTGAGGACAGCAGGTCCCCAGGCAGGAGCACCC  
 MetSerAspGluAspSerCysValAlaCysGlySerLeuArgThrAlaGlyProGlnAlaGlyAlaPro  
 801  
 TCCCCATGGCCCTGGGAGGCCAGGCTGATGCACCAGGGACAGCTGGCCTGTGGCGGAGCCCTGGTGTGAGAGGAGGCGGT  
 SerProTrpProTrpGluAlaArgLeuMetHisGlnGlyGlnLeuAlaCysGlyGlyAlaLeuValSerGluGluAlaVa  
 881  
 GCTAACTGCTGCCCCACTGCTTCATTGGGCGCCAGGCCCCAGAGGAATGGAGCGTAGGGCTGGGGACCAGACCGGAGGAGT  
 lLeuThrAlaAlaHisCysPheIleGlyArgGlnAlaProGluGluTrpSerValGlyLeuGlyThrArgProGluGluT  
 961  
 GGGGCCTGAAGCAGCTCATCCTGCATGGAGCCTACACCCACCCTGAGGGGGGCTACGACATGGCCCTCCTGCTGCTGGCC  
 rpGlyLeuLysGlnLeuIleLeuHisGlyAlaTyrThrHisProGluGlyGlyTyrAspMetAlaLeuLeuLeuAla  
 1041  
 CAGCCTGTGACACTGGGAGCCAGCCTGCGGCCCTCTGCCTGCCCTATGCTGACCACCACCTGCCTGATGGGAGCGTGG  
 GlnProValThrLeuGlyAlaSerLeuArgProLeuCysLeuProTyrAlaAspHisHisLeuProAspGlyGluArgGl  
 1121  
 CTGGGTTCCTGGGACGGGCCCCGCCAGGAGCAGGCATCAGCTCCCTCCAGACAGTGCCCGTGACCTCCTGGGGCCTAGGG  
 yTrpValLeuGlyArgAlaArgProGlyAlaGlyIleSerSerLeuGlnThrValProValThrLeuLeuGlyProArgA  
 1201  
 CCTGCAGCCGGCTGCATGCAGCTCCTGGGGGTGATGGCAGCCCTATTCTGCCGGGGATGGTGTGTACCAGTGCTGTGGGT  
 laCysSerArgLeuHisAlaAlaProGlyGlyAspGlySerProIleLeuProGlyMetValCysThrSerAlaValGly  
 1281  
 GAGCTGCCCAGCTGTGAGGTGAGCCCCAGGCCCCACACCTTACCTAACAGGCCCTGGCATCCCCTCACCCAATAGCTC  
 GluLeuProSerCysGluValSerProArgProProHisLeuThr  
 1361  
 AAGAACGGACCTTCCAGGCTTGGCCTCTGGACCCACCTCCACCTGAAGCTAAGCCTTTTTGCCAATTAGCCCCCAAACA  
 1441  
 GCCAG

Fig. 8

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1 CTTAACAGCCACTTGTTTTCATCCCACCTGGGCATTAGGTTGACTT  
 46 CAAAGATGCCTCAGTTACTGCAAAACATTAATGGGATCATCGAGG  
 MetProGlnLeuLeuGlnAsnIleAsnGlyIleIleGluA  
 91 CCTTCAGGCGCTATGCAAGGACGGAGGGCAACTGCACAGCGCTCA  
 laPheArgArgTyrAlaArgThrGluGlyAsnCysThrAlaLeuT  
 136 CCCGAGGGGAGCTGAAAAGACTCTTGGAGCAAGAGTTTGCCGATG  
 hrArgGlyGluLeuLysArgLeuLeuGluGlnGluPheAlaAspV  
 181 TGATTGTGAAACCCACGATCCAGCAACTGTGGATGAGGTCCTGC  
 alIleValLysProHisAspProAlaThrValAspGluValLeuA  
 226 GTCTGCTGGATGAAGACCACACAGGGACTGTGGAATTCAAGGAAT  
 rgLeuLeuAspGluAspHisThrGlyThrValGluPheLysGluP  
 271 TCCTGGTCTTAGTGTTTAAAGTTGCCCAGGCCTGTTTCAAGACAC  
 heLeuValLeuValPheLysValAlaGlnAlaCysPheLysThrL  
 316 TGAGCGAGAGTGCTGAGGGAGCCTGCGGCTCTCAAGAGTCTGGAA  
 euSerGluSerAlaGluGlyAlaCysGlySerGlnGluSerGlyS  
 361 GCCTCCACTCTGGGGCCTCGCAGGAGCTGGGCGAAGGACAGAGAA  
 erLeuHisSerGlyAlaSerGlnGluLeuGlyGluGlyGlnArgS  
 406 GTGGCACTGAAGTGGGAAGGGCGGGGAAAGGGCAGCATTATGAGG  
 erGlyThrGluValGlyArgAlaGlyLysGlyGlnHisTyrGluG  
 451 GGAGCAGCCACAGACAGAGCCAGCAGGGTTCCAGAGGGCAGAACAA  
 lySerSerHisArgGlnSerGlnGlnGlySerArgGlyGlnAsnA  
 496 GGCCTGGGGTTCAGACCCAGGGTCAGGCCACTGGCTCTGCGTG  
 rgProGlyValGlnThrGlnGlyGlnAlaThrGlySerAlaTrpV  
 541 TCAGCAGCTATGACAGGCAAGCTGAGTCCCAGAGCCAGGAAAGAA  
 alSerSerTyrAspArgGlnAlaGluSerGlnSerGlnGluArgI  
 586 TAAGCCCGCAGATACAACCTCTCTGGGCAGACAGAGCAGACCCAGA  
 leSerProGlnIleGlnLeuSerGlyGlnThrGluGlnThrGlnL  
 631 AAGCTGGAGAAGGCAAGAGGAATCAGACAACAGAGATGAGGCCAG  
 ysAlaGlyGluGlyLysArgAsnGlnThrThrGluMetArgProG  
 676 AGAGACAGCCACAGACCAGGGAACAGGACAGAGCCCACCAGACAG  
 luArgGlnProGlnThrArgGluGlnAspArgAlaHisGlnThrG

Fig. 9

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721 GTGAGACTGTGACTGGATCTGGAAGTCAGACCCAGGCAGGTGCCA  
 lyGluThrValThrGlySerGlyThrGlnThrGlnAlaGlyAlaT  
 766 CCCAGACTGTGGAGCAGGACAGCAGCCACCAGACAGGAAGCACCA  
 hrGlnThrValGluGlnAspSerSerHisGlnThrGlySerThrS  
 811 GCACCCAGACACAGGAGTCCACCAATGGCCAGAACAGAGGGACTG  
 erThrGlnThrGlnGluSerThrAsnGlyGlnAsnArgGlyThrG  
 856 AGATCCACGGTCAAGGCAGGAGCCAGACCAGCCAGGCTGTGACAG  
 luIleHisGlyGlnGlyArgSerGlnThrSerGlnAlaValThrG  
 901 GAGGACACACTCAGATACAGGCAGGGTCACACACCCGAGACTGTGG  
 lyGlyHisThrGlnIleGlnAlaGlySerHisThrGluThrValG  
 946 AGCAGGACAGAAGCCAAACTGTAAGCCACGGAGGGGCTAGAGAAC  
 luGlnAspArgSerGlnThrValSerHisGlyGlyAlaArgGluG  
 991 AGGGACAGACCCAGACGCAGCCAGGCAGTGGTCAAAGATGGATGC  
 lnGlyGlnThrGlnThrGlnProGlySerGlyGlnArgTrpMetG  
 1036 AAGTGAGCAACCCTGAGGCAGGAGAGACAGTACCGGGAGGACAGG  
 lnValSerAsnProGluAlaGlyGluThrValProGlyGlyGlnA  
 1081 CCCAGACTGGGGCAAGCACTGAGTCAGGAAGGCAGGAGTGGAGCA  
 laGlnThrGlyAlaSerThrGluSerGlyArgGlnGluTrpSerS  
 1126 GCACTCACCCAAGGCGCTGTGTGACAGAAGGGCAGGGAGACAGAC  
 erThrHisProArgArgCysValThrGluGlyGlnGlyAspArgG  
 1171 AGCCACACAGTGGTTGGTGAGGAATGGGTTGATGACCACTCAAGGG  
 lnProThrValValGlyGluGluTrpValAspAspHisSerArgG  
 1216 AGACAGTGATCCTCAGGCTGGACCAGGGCAACTTGCATACCAGTG  
 luThrValIleLeuArgLeuAspGlnGlyAsnLeuHisThrSerV  
 1261 TTTCTCAGCACAGGGCCAGGATGCAGCCCAGTCAGAAGAGAAGC  
 alSerSerAlaGlnGlyGlnAspAlaAlaGlnSerGluGluLysA  
 1306 GAGGCATCACAGCTAGAGAGCTGTATTCCTACTTGAGAAGCACCA  
 rgGlyIleThrAlaArgGluLeuTyrSerTyrLeuArgSerThrL  
 1351 AGCCATGACTTCCCCGACTCCAATGTCCAGTACTGGAAGAAGACA  
 ysPro  
 1396 GCTGGAGAGAGTTTGGCTTGTCTGCATGGCCAATCCAGTGGGTG  
 1441 CATCCCTGGACATCAGCTCTTCATTATGCAGCTTCCCTTTTAGGT  
 1486 CTTTCTCAATGAGATAATTTCTGCAAGGAGCTTTCTATCCTGAAC  
 1531 TCTTCTTTCTTACCTGCTTTGCGGTGCAGACCTCTCAGGAGCAG  
 1576 GAAGACTCAGAACAAGTCACCCCTT

Fig. 9 (continued)

1. 116181300.0.184\_Cura\_108  
2. 116181300.0.27\_Cura\_56

116181300184\_cura\_108 MSDEDSVACGSLRTAGPQAGAPSPWPWEARLMHQQLACGGALVSEEA VLTAAHCFIIGR  
11618130027\_cura\_56 MSDEDSVACGSLRTAGPQAGAPSPWPWEARLMHQQLACGGALVSEEA VLTAAHCFNNGR

116181300184\_cura\_108 QAPEEWSVGLGTRPPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLCLLPYA  
11618130027\_cura\_56 QAPEEWSVGLGTRPPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRALLCLPYF

116181300184\_cura\_108 DHHLPDGERGWVLGRARPGAGISSLQTVPTLLGPRACSRRLHAAPGGDGSPIILPGMVCTS  
11618130027\_cura\_56 DHHLPDGERGWVLGRARPGAGISSLQTVPTLLGPRACSRRLHAAPGGDGSPIILPGMVCTS

116181300184\_cura\_108 AVGELPSCEVSPRPPIHUT  
11618130027\_cura\_56 AVGELPSCEGLSGAPLHHEVRGTWFLAGLHSFGDACQGPAPPAVFTALPAYEDWVSSLDW

116181300184\_cura\_108 ~~~~~  
11618130027\_cura\_56 QVYFAEEPEPEAEPGSCLANISQPTSC

Fig. 10

Sequences analyzed:

1. 14578444-0-47\_Cura\_56
2. 14578444-0-143Cura\_56

14578444047_cura_56	MEKMLAGCFLLILGQIVLLP	CEARERSGRSISRGRHARTHPTALLESSCENKRADLVF
145784440143_cura_56	MEKMLAGCFLLILGQIVLLP	CEARERSGRSISRGRHARTHPTALLESSCENKRADLVF
14578444047_cura_56	IIDSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFKRKSEV	
145784440143_cura_56	IIDSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFKRKSEV	
14578444047_cura_56	ERAVKRMRLSTGTMGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTDGRPQDSVAEV	
145784440143_cura_56	ERAVKRMRLSTGTMGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTDGRPQDSVAEV	
14578444047_cura_56	AAKARDTGILIFAIGVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAH	
145784440143_cura_56	AAKARDTGILIFAIGVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAH	
14578444047_cura_56	MCSTLEHNCAHFCINIPGSYVCRCKQGYILNSDQTTTCRIQDLCAMEDHNCEQLCVNVPGS	
145784440143_cura_56	MCSTLEHNCAHFCINIPGSYVCRCKQGYILNSDQTTTCRIQDLCAMEDHNCEQLCVNVPGS	
14578444047_cura_56	FVCECYSGYALAEDGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTC	
145784440143_cura_56	FVCECYSGYALAEDGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTC	

Fig. 11

14578444047_cura_56	KIDYCASSNHGCGQYECVNTDDSYSCHCLKGFTLNPDKKTCRRINICALNKPGEHECVNM
145784440143_cura_56	KIDYCASSNHGCGQYECVNTDDSYSCHCLKGFTLNPDKKTCRRINICALNKPGEHECVNM
14578444047_cura_56	EESYYCRCHRGYTLDPNGKPCSRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLLINEDLK
145784440143_cura_56	EESYYCRCHRGYTLDPNGKPCSRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLLINEDLK
14578444047_cura_56	TCSRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRS DGKTC AKLDSCALGDHGCEHSC
145784440143_cura_56	TCSRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRS DGKTC AKLDSCALGDHGCEHSC
14578444047_cura_56	VSEDSFVCQCFFEGYILREDGKTCRRRKDVCAIDHGCEHICVNSDDSYTCECLEGFRLTE
145784440143_cura_56	VSEDSFVCQCFFEGYILREDGKTCRRRKDVCAIDHGCEHICVNSDDSYTCECLEGFRLTE
14578444047_cura_56	DGKRRCRISSGKDVCKSTHHGCEHICVNNGNSYICKCSEGFVLAEDGRRCKKCTEGPIDLV
145784440143_cura_56	DGKRRCRISSGKDVCKSTHHGCEHICVNNGNSYICKCSEGFVLAEDGRRCKKCTEGPIDLV
14578444047_cura_56	FVIDGSKSLGEENFEVVKQFVTGIIDSLTISPKAARVGLLQYSTQVHTEFTLRNFNSAKD
145784440143_cura_56	FVIDGSKSLGEENFEVVKQFVTGIIDSLTISPKAARVGLLQYSTQVHTEFTLRNFNSAKD
14578444047_cura_56	MKKAVAHMKYMGKGSMTGLALKHMFERSFTQGEGARPFSTRVPRAAIVFTDGRNQDDVSE
145784440143_cura_56	MKKAVAHMKYMGKGSMTGLALKHMFERSFTQGEGARPLFKKGAQSSHCVHRRTGSG~~~~
14578444047_cura_56	WASKAKANGITMYAVGVGKAIEEELQEIASOPTNKHLYAEDFSTMDEISEKLKKGICEA
145784440143_cura_56	~~~~~
14578444047_cura_56	LEDSDGRQDSPAGELPKTVQQPTESEPTVINIQDLLSCSNFAVQHRYLFEEDNLLRSTQK
145784440143_cura_56	~~~~~
14578444047_cura_56	LSHSTKPSGSPLEEKHDQCKENLIMFQNLANEVVRKLTQRLEEMTQRMALLENRLRYR
145784440143_cura_56	~~~~~

Fig. 11 (continued)

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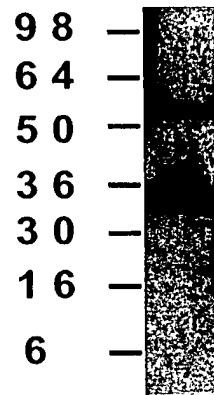


Fig. 12

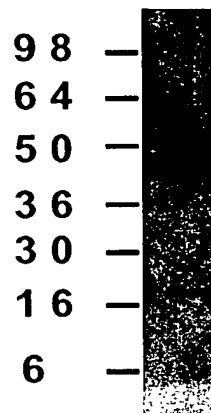


Fig. 13



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Normal & Tumor Tissues	11696905	16406477.0.206	21433858	21637262.0.64
Endothelial cells	3.5	0.0	6.6	0.0
Endothelial cells (treated)	2.9	0.0	2.0	0.0
Pancreas	9.4	3.1	1.2	0.0
Pancreatic ca. CAPAN 2	3.7	0.0	0.3	0.0
Adipose	60.7	0.3	22.5	0.8
Adrenal gland	18.0	0.0	3.2	0.2
Thyroid	13.8	0.0	4.6	2.4
Salivary gland	0.0	0.6	0.7	36.3
Pituitary gland	2.2	0.6	4.0	1.4
Brain (fetal)	3.1	0.5	6.9	0.7
Brain (whole)	4.4	0.7	24.5	0.3
Brain (amygdala)	17.2	0.1	5.0	0.4
Brain (cerebellum)	1.6	1.2	41.8	1.4
Brain (hippocampus)	9.3	0.8	10.4	0.6
Brain (hypothalamus)	5.7	10.0	2.3	0.5
Brain (substantia nigra)	33.2	0.7	5.2	0.1
Brain (thalamus)	22.7	0.5	5.2	0.0
Spinal cord	21.8	0.3	4.0	1.5
CNS ca. (glio/astro) U87-MG	2.2	0.0	1.0	0.0
CNS ca. (glio/astro) U-118-MG	4.5	0.0	1.5	0.0
CNS ca. (astro) SW1783	0.0	0.0	0.7	0.0
CNS ca.* (neuro; met) SK-N-AS	2.7	0.0	12.6	0.1
CNS ca. (astro) SF-539	0.2	0.0	0.0	0.0
CNS ca. (astro) SNB-75	1.3	0.0	0.6	0.0
CNS ca. (glio) SNB-19	0.6	0.0	0.8	0.2
CNS ca. (glio) U251	0.2	0.0	3.6	0.1
CNS ca. (glio) SF-295	6.2	0.1	0.2	0.0
Heart	10.7	0.1	1.3	0.1
Skeletal muscle	18.4	0.0	0.2	0.2
Bone marrow	11.1	0.0	0.1	0.0
Thymus	7.3	0.9	2.5	0.5
Spleen	2.9	0.1	1.4	0.0
Lymph node	4.3	0.1	1.3	0.1

Fig. 14

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Normal & Tumor Tissues	11696905	16406477.0.206	21433858	21637262.0.64
Colon (ascending)	1.3	0.2	5.1	1.3
Stomach	5.4	0.2	5.7	0.0
Small intestine	7.0	0.2	1.7	0.0
Colon ca. SW480	0.4	0.0	0.0	0.1
Colon ca.* (SW480 met)SW620	0.1	0.0	0.0	0.0
Colon ca. HT29	0.4	0.0	0.0	0.1
Colon ca. HCT-116	4.4	0.0	0.0	0.0
Colon ca. CaCo-2	1.1	0.1	0.1	0.0
Colon ca. HCT-15	11.0	0.2	0.3	0.2
Colon ca. HCC-2998	0.0	0.0	1.3	0.0
Gastric ca.* (liver met) NCI-N87	4.9	0.3	1.9	0.0
Bladder	18.8	0.1	10.8	0.1
Trachea	4.8	0.0	2.2	100.0
Kidney	7.3	0.4	13.1	0.1
Kidney (fetal)	11.0	1.8	29.5	0.1
Renal ca. 786-0	0.4	0.0	0.0	0.0
Renal ca. A498	56.3	0.0	0.0	0.1
Renal ca. RXF 393	2.7	0.0	0.1	0.0
Renal ca. ACHN	1.0	0.0	0.1	0.1
Renal ca. UO-31	1.8	0.0	0.4	0.1
Renal ca. TK-10	13.4	0.5	0.2	0.1
Liver	74.7	0.7	2.1	0.1
Liver (fetal)	27.7	1.2	0.9	0.0
Liver ca. (hepatoblast HepG2	7.4	0.0	0.0	0.0
Lung	9.9	0.0	2.9	0.0
Lung (fetal)	1.5	1.5	3.0	0.0
Lung ca. (small cell) LX-1	0.4	0.0	0.0	0.0
Lung ca. (small cell) NCI-H69	0.5	0.1	9.3	0.5
Lung ca. (s.cell var.) SHP-77	0.6	0.4	100.0	1.7
Lung ca. (large cell) NCI-H460	20.6	0.3	66.9	0.6
Lung ca. (non-sm. cell) A549	3.3	0.0	15.5	0.1
Lung ca. (non-s.cell) NCI-H23	7.4	0.5	9.0	0.0
Lung ca (non-s.cell) HOP-62	32.1	0.1	1.5	0.1
Lung ca. (non-s.cl) NCI-H522	11.0	0.6	0.0	0.0
Lung ca. (squam.) SW 900	3.3	0.9	6.1	0.1

Fig. 14 (continued)

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Normal & Tumor Tissues	11696905.0	16406477.0.206	21433858.0	21637262.0.64
Mammary gland	30.4	1.5	12.2	0.0
Breast ca.* (pl. effusion) MCF-7	4.8	0.0	0.0	0.0
Breast ca.* (pl.ef) MDA-MB-231	2.2	0.0	0.0	0.1
Breast ca.* (pl. effusion) T47D	9.8	0.1	0.9	0.6
Breast ca. BT-549	9.2	0.1	1.2	0.3
Breast ca. MDA-N	1.3	0.0	0.0	0.0
Ovary	6.0	0.3	9.7	0.0
Ovarian ca. OVCAR-3	1.6	0.1	0.8	0.1
Ovarian ca. OVCAR-4	1.9	0.0	0.0	0.0
Ovarian ca. OVCAR-5	7.1	0.3	6.9	0.6
Ovarian ca. OVCAR-8	1.3	2.7	2.7	0.0
Ovarian ca. IGROV-1	0.7	0.2	5.0	0.0
Ovarian ca.* (ascites) SK-OV-3	2.5	0.0	0.2	0.0
Myometrium	2.3	0.0	41.2	1.2
Uterus	6.3	0.6	25.7	0.1
Placenta	100.0	0.0	94.0	0.1
Prostate	13.3	0.1	3.4	0.1
Prostate ca.* (bone met) PC-3	7.9	1.7	0.2	0.2
Testis	14.3	100.0	37.1	4.0
Melanoma Hs688(A).T	1.4	0.0	0.0	0.0
Melanoma* (met) Hs688(B).T	5.3	0.0	0.0	0.0
Melanoma UACC-62	0.6	0.0	0.0	0.0
Melanoma M14	0.9	0.1	0.3	0.2
Melanoma LOX IMVI	1.0	0.0	0.0	0.1
Melanoma* (met) SK-MEL-5	0.0	0.0	8.7	0.0
Melanoma SK-MEL-28	100.0	0.0	0.0	0.0

Fig. 14 (continued)

## Drawings

**Figure 15. Nucleotide Sequence for CG106318-01.**

```
>CG106318-01 4810 nt
GTCCATGGGGCCGATGTATGGGAGATGAATGTGGTCCCCGAGGCATCCAAACGAGGGCTG
TGTGGTGTGCTCATGTGGAGGGATGGACTACACTGCATACTAACTGTAAGCAGGCCGAGA
GACCCAATAACCAGCAGAATTGTTTCAAAGTTTGGCATTGGCACAAAGAGTTGTACGACT
GGAGACTGGGACCTTGGAATCAGTGTGAGCCCGTGATTTCAAAAAGCCTAGAGAAACCTC
TTGAGTGCATTAAAGGGGGAAGAAGGTATTAGGTGAGGGAGATAGCGTGCATCCAGAAAG
ACAAAGACATTCCTGCGGAGGATATCATCTGTGAGTACTTTGAGCCCAAGCCTCTCCTGG
AGCAGGCTTGCTCATTCTTCCAGCAAGATTGCATCGTGTCTGAATTTTCTGCCTGGT
CCGAATGCTCCAAGACCTGCGGCAGCGGGCTCCAGCACCAGGACGCGTCAATGTGGTGGCGC
CCCCGACGTTGCGGAGGCTCTGGCTGTCCAAACCTGACGGAGTTCCAGGTGTGCCAATCCA
GTCCATGCGAGGCCGAGGACCTCAGGTACAGCCTGCATGTGGGGCCCTGGAGCACCTGCT
CAATGCCCACTCCCAGCAAGTAAGACAAGCAAGGAGACGCGGGAAGAATAAAGAACGGG
AAAAGGACCCGAGCAAGGAGTAAAGGATCCAGAAAGCCCGCAGCTTATTAAGAAAAAGA
GAAACAGAAACAGGCAAGACAGACAAGAGAACAATATTGGGACATCCAGATTGGATATC
AGACCAGAGAGGTTATGTGCATTAACAAGACGGGGAAAGCTGCTGATTTAAGCTTTTGCC
AGCAAGAGAGCTTCCATGACCTTCCAGTCTGTGTGATACCAAAAGAGTGCCAGGTTT
CCGAGTGGTCAGAGTGGAGCCCCTGCTCAAAAACATGCCATGACATGGTGTCCCCTGCAG
GCACCTGTGTAAGGACACGAAACCATCAGGCAGTTTCCCATTGGCAGTGAAGAGGAGTGTG
CAGAAATTTGAAGAAAAAGAACCTGTTTGTCTCAAGGAGATGGAGTTGTCCCCTGTGCCA
CGTATGGCTGGAGAACTACAGAGTGGAGTGGCTGTGGACCCCTTGTCTCAGTCAGC
AGGACAAGAGGCGCGGCAACAGACGGCCCTCTGTGGAGGGGGCATCCAGACCCGAGAGG
TGTACTGCGTGCAGGCCAACGAAAACCTCCTCTCACAATTAAGTACCCACAAGAACAAAG
AAGCCTCAAAGCCAAATGGACTTAAATATGCACTGGACCTATCCCTAATACTACACAGC
TGTGCCACATTCCTTGTCCAACCTGAATGTGAAGTTTCACTTGGTCACTTGGGGACCTT
GTACTTATGAAAACCTGAATGATCAGCAAGGGAAAAAGGCTTCAAACCTGAGGAAGCGGC
GCATTACCAATGAGCCCACTGGAGGCTCTGGGGTAACCGGAAACTGCCCTCACTTACTGG
AAGCCATTCCCTGTGAAGAGCCTGCCTGTTATGACTGGAAAGCGGTGAGACTGGGAGACT
GCGAGCCAGATAACGGAAAGGAGTGTGGTCCAGGCACGCAAGTTCAAGAGGTTGTGTGCA
TCAACAGTGATGGAGAAGAGTTGACAGACAGCTGTGACAGAGATGCCATCTTCCCCATCC
CTGTGGCCTGTGATGCCCCATGCCCGAAAGACTGTGTGCTCAGCACATGGTCTACGTGGT
CCTCCTGCTCACACAGCTGCTCAGGGAAAAACGACAGAAGGGAAACAGATACGAGCACGAT
CCATTCTGGCCTATGCGGGTGAAGAAGGTGGAATTCGCTGTCCAAATAGCAGTGCTTTGC
AAGAAGTACGAAGCTGTATGAGCATCCTTGACAGTGTAACCACTGGCAAACCTGGTCCCT
GGGGCCAGTGCAATGAGGACCTCAGTATCGTCTTCAACACAACCTACGACTTGGAAATG
GGGAGGCCCTCCTGCTCTGTGCGCATGCAGACAAGAAAAGTCATCTGTGTGCGAGTCAATG
TGGGCCAAGTGGGACCCAAAAATGTCTGAAAGCCTTCGACCTGAAACTGTAAGGCCTT
GTGCTTCTCCTTGTGAAGAAGGACTGATTGTGACCCCATATAGTACTGGACATCATGCC
CCTCTTGTGTAAAGAGGGGACTCCAGTATCAGGAAGCAGTCTAGGCATCGGGTCACTCA
TTCAGCTGCCAGCCAACGGGGGCCGAGACTGCACAGATCCCCTCTATGAAGAGAAGGCCT
GTGAGGCACCTCAAGCGTGCCAAAGCTACAGGTGGAAGACTCACAAATGGCGCAGATGCC
AATTAGTCCCTTGGAGCGTGCAACAAGACAGCCCTGGAGCACAGGAAGGCTGTGGGCCTG
GGCGACAGGCAAGAGCCATTACTTGTGCAAGCAAGATGGAGGACAGGCTGGAATCCATG
AGTGCCATACAGTATGCAGGCCCTGTGCCAGCCCTTACCCAGGCCTGCCAGATCCCCTGCC
AGGATGACTGTCAATTGACCAGCTGGTCCAAGTTTCTTCATGCAATGGAGACTGTGGTG
CAGTTAGGACCAGAAAGCGCACTCTTGTGGAAAAAGTAAAAAGAAGGAAAAATGTAAAA
ATTCCCATTTGTATCCCCTGATTGAGACTCAGTATTGTCCTTGTGACAAATATAATGCAC
AACCTGTGGGGAACCTGGTCACTGTATTTTACCAGAGGGAAAAAGTGAAGTGTGCTGG
GAATGAAAGTACAAGGAGACATCAAGGAATGCGGACAAGGATATCGTTACCAAGCAATGG
CATGCTACGATCAAATGGCAGGCTTGTGGAACATCTAGATGTAACAGCCATGGTTACA
TTGAGGAGGCCTGCATCATCCCCTGCCCTCAGACTGCAAGCTCAGTGAGTGGTCCAAC
GGTCGCGCTGCAGCAAGTCCCTGTGGGAGTGGTGTGAAGGTTTCGTTCTAAATGGCTGCGTG
AAAAACCATATAATGGAGGAAGGCCTTCCCCAACTGGACCATGTCAACCAGGCACAGG
TGTATGAGGTTGTCCCATGCCACAGTGAAGTCAACCAAGTACCTATGGGTACAGAGCCCT
GGAGCATCTGCAAGGTGACCTTTGTGAATATGCGGGAGAAGTGTGGAGAGGGCGTGCAAA
CCCCAAAAGTGAGATGCATGCAGAATACAGCAGATGGCCCTTCTGAACATGTAGAGGATT
ACCTCTGTGACCCAGAGAGATGCCCTGGGCTCTAGAGTGTGCAAAATACCATGCCCTG
AGGACTGTGTGATATCTGAATGGGGTCCATGGACCCAATGTGTTTGCCTTGCAATCAA
GCAGTTTCCGGCAAAAGGTCACTGATCCCATCAGACAACAGCTGATGAAGGAAGATCTT
GCCCTAATGCTGTTGAGAAAGAACCCTGTAACCTGAACAAAAACTGCTACCACTATGATT
ATAATGTAACAGACTGGAGTACATGTCAGCTGAGTGAGAAGGCAGTTTGTGGAAATGGAA
TAAAAACAAGGATGTTGGATTGTGTTTCAAGTGATGGCAAGTCAGTTGACCTGAAATATT
```

GTGAAGCGCTTGGCTTGGAGAAGAACTGGCAGATGAACACGTCCTGCATGGTGGAAATGCC  
 CTGTGAACTGTCAGCTTCTGATTGGTCTCCTTGGTCAGAATGTTCTCAAACATGTGGCC  
 TCACAGGAAAAATGATCCGAAGACGAACAGTGACCCAGCCCTTCAAGGTGATGGAAGAC  
 CATGCCCTTCCCTGATGGACCAAGTCCAAACCTGCCCAAGTGAAGCCTTGTATCGGTGGC  
 AATATGGCCAGTGGTCTCCATGCCAAGTGCAGGAGGCCCAAGTGTGGAGAAGGGACCAGAA  
 CAAGGAACATTCTTGTGTAGTAAGTGATGGGTGAGCTGATGATTTACGCAAAAGTGGTGG  
 ATGAGGAATTCTGTGCTGACATTGAACTCATTATAGATGGTAATAAAATATGGTTCTGG  
 AGGAATCCTGCAGCCAGCCTTGCCCAAGGTGACTGTTATTTGAAGGACTGGTCTTCTCTGGA  
 GCCTGTGTGTCAGCTGACCTGTGTGAATGGTGAGGATCTAGGCTTTGGTGGAAATACAGGTCA  
 GATCCAGACCGGTGATTATACAAGAACTAGAGAATCAGCATCTGTGCCCAGAGCAGATGT  
 TAGAAACAAAATCATGTTATGATGGACAGTGCTATGAATATAAATGGATGGCCAGTGCTT  
 GGAAGGGCTCTTCCCGAACAGTGTGGTGTCAAAGGTGAGATGGTATAAATGTAACAGGGG  
 GCTGCTTGGTGATGAGCCAGCCTGATGCCGACAGGTCTTGTAAACCCACCGTGTAGTCAAC  
 CCCACTCGTACTGTAGCGAGACAAAACATGCCATTGTGAAGAAGGGTACACTGAAGTCA  
 TGTCTTCTAACAGCACCTTGAGCAATGCACACTTATCCCCGTGGTGGTATTACCCACCA  
 TGGAGGACAAAAGAGGAGATGTGAAAACCAAGTCGGGCTGTACATCCAACCCAACCTCCA  
 GTAACCCAGCAGGACGGGGAAGGACCTGGTTTCTACAGCCATTTGGGCCAGATGGGAGAC  
 TAAAGACCTGGGTTTACGGTGTAGCAGCTGGGGCATTTGTGTTACTCATCTTTATTGTCT  
 CCATGATTTATCTGATTCGAAAAAGCCAAAGAAACCCCAAGAAGGCCAAACAACCGAC  
 TGAACCTTTAACCTTAGCCTATGATGGAGATGCCGACATGTAACATATAACTTTTCTG  
 GCAACAACCA (SEQ ID NO: 40)

Protein Sequence for CG106318-01 ORF Start: 18 ORF Stop: 4782 Frame: 3

Protein Sequence:

>CG106318-01-prot 1588 aa  
 MGDECGPGGIQTRAVWCAHVEGWTTLHTNCKQAERPNNQONCFKVCODWHKELYDWRLGPW  
 NQCQPVISKSLEKPLECIKGEEGIQVREIACIQKDKDIPAEIICEYFEPKPLLEQACLI  
 PCQQDCIVSEFSAWSECSKTCGSLQHRTRHVVAPPQFGSGCPNLTEFQVCQSSPCEAE  
 ELRYSLHVGPWSTCSMPHSRQVRQARRRGKNKEREKDRSKGVKDPEARELIKKNRNRNRQ  
 NRQENKYWDIQIGYQTRVEMCINKTGKAADLSFCQKEKLPMTFQSCVITKECQVSEWSEW  
 SPCSKTCHDMVSPAGTRVTRTIRQFPIGSEKECFEFEEKEPCLSQGDGVVPCATYGWRT  
 TEWTECRVDPLLSQQDKRRGNQALCGGGIQTREVVYCVQANENLLSQLSTHKNKEASKPM  
 DLKLTGPIPNNTQLCHIPCTECEVSPWSAWGPCTYENCNDQQGKKGFKLRKRRTNEP  
 TGGSGVTGNCPHLLAIPCEEPACYDWKAVRLGDCEPDNGKECGPGTQVQEVVCINSDE  
 EVDRQLCRDAIFPIPVACDAPCPKDCVLTSTWSTWSSCSHTCSGKTTEGKQIRARSILAYA  
 GEEGGIRCPNSSALQEVRSNEHPCTVYHWQTGPWGQCIEDTSVSSFNTTTTWNGEASCS  
 VGMQTRKVICVRVNVGQVGPKKCPESLRPETVRPCLLPCKKDCIVTPYSDWTSCPSSCKE  
 GDSSIRKQSRHRVLIQLPANGGRDCTDPLYEEKACEAPQACQSYRWKTHKWRRRCQLVPWS  
 VQQDSPGAQEGCGPGRQARAITCRKQDGGQAGIHECLQYAGVPALTQACQIPQDDCQL  
 TWSKFSSCNGDCGAVRTRKRTLVGKSKKKECKNSHLYPLIETQYCPCKYNAQPVGNW  
 SDCILPEGKVEVLLGMKVQGDKECGQGYRYQAMACYDQNGRLVETSRCSNHHGYIEEACI  
 IPCPSDCKLSEWSNWSRCSKSCGSGVKVRSKWLREKPYNGGRPCPKLDHVNQAQVYEVVP  
 CHSDCNQYLWVTEPWSICKVTFVNMRENCGEVQTRKVRMCMQNTADGPSEHVEDYLCDPE  
 EMPLGSRVCKLPCPEDCVISEWGPWTQCVLPCNQSSFRQRSADPIRQPADEGRSCPNAVE  
 KEPCLNKNKCYHYDYNVDWSTCQLSEKAVCGNGIKTRMLDCVRSDGKSVDLKYCEALGL  
 EKNWQMNTSCMVECPVNCQLSDWSPWSECSQTCGLTGKMIRRRRTVTQPFQGDGRPCPSLM  
 DQSKPCPVKPCYRWQYQWSPCQVQEAQCGEGTRTRNISCVVSDGSADDFSKVVDEEFCA  
 DIELIIDGNKNMVLSESCQPCPGDCYLKDWSSWSLQCLTCVNGEDLGFGGIQRVSRPVI  
 IQELENQHLCPQMLETSCYDGQCYEYKWMASAWKGSRTVWCQRSDGINVTGGCLVMS  
 QPDADRSCNPPCSQPHSYCSETKTCHCEEGYTEVMSSNSTLEQCTLIPVVVLPTMEDKRG  
 DVKTSRAVHPTQPSNPAGRGRTWFLQPFQPDGRLKTWVYGVAAGAFVLLIFIVSMIYLA  
 CKKPKKPQRRQNNRLKPLTLAYDGDADM (SEQ ID NO: 41)

**Figure 16. Nucleotide and Protein Sequences for CG50817-04.**

>CG50817-04 1447 nt

GCGGACACCAGTGATGCTCCTGGGACCCTACGCAATCTGCGCCTGCGTCTCATCAGTCGC  
 CCCACATGTAAGTGTATCTACAACCAGCTGCACCAGCGACACCTGTCCAACCCGGCCCGG  
 CCTGGGATGCTATGTGGGGGCCCCAGCCTGGGGTGCAGGGCCCCCTGTCAGGTCTGATAG  
 GGAGAAGAGAAGGAGCAGAAGGGGAGGGGCCCTAACCTGGGCTGGGGGTGGACTCACAG  
 GACTGGGGGAAAGAGCTGCAATCAGAGGGTGTCTGCCATAGCTGGGCTCAGGCATCTGTC  
 CTTGGCTTTGTTGCCTGGCTCCAGGGAGATTCCGGGGGCCCTGTGCTGTGCCTCGAGCCT  
 GACGGACACTGGGTTGAGGCTGGCATCATCAGCTTTCATCAAGCTGTGCCAGGAGGAC  
 GCTCCTGTGCTGCTGACCAACACAGCTGCTCACAGTTCCTGGCTGCAGGCTCGAGTTCAG  
 GGGGCAGCTTTCCTGGCCCAGAGCCCAGAGACCCCGGAGATGAGTGATGAGGACAGCTGT  
 GTAGCCTGTGGATCCTTGAGGACAGCAGGTCCCCAGGCAGGAGCACCTCCCCATGGCCC  
 TGGGAGGCCAGGCTGATGCACCAGGGACAGCTGGCCTGTGGCGGAGCCCTGGTGTGAGAG  
 GAGGCGGTGCTAACTGCTGCCACTGCTTCATTGGGCGCCAGGCCCCAGAGGAATGGAGC  
 GTAGGGCTGGGGACCAGACCGGAGGAGTGGGGCCTGAAGCAGCTCATCCTGCATGGAGCC  
 TACACCCACCCTGAGGGGGGCTACGACATGGCCCTCCTGCTGCTGGCCCAGCCTGTGACA  
 CTGGGAGCCAGCCTGCGGCCCTCTGCCTGCCCTATGCTGACCACCACCTGCCTGATGGG  
 GAGCGTGGCTGGGTTCTGGGACGGGCCCGCCCAGGAGCAGGCATCAGCTCCCTCCAGACA  
 GTGCCCGTGACCCTCCTGGGGCCTAGGGCCTGCAGCCGGCTGCATGCAGCTCCTGGGGGT  
 GATGGCAGCCCTATTCTGCCGGGGATGGTGTGTACCAAGTGTGTGGGTGAGCTGCCAGC  
 TGTGAGGCCAACCAACCAGCTGCTGACAGGGGACCTGGCCATTCTCAGGAACAAGAGAAT  
 GCAGGCAGGCAATGGCATTACTGCCCTGTCTCCTCCCCACCCTGTCTGTGTGATTCCAG  
 GCACCAGGGCAGGCCAGAGCCAGAGCTGTGGGAAGGAACCTGCCTGGGGCCACAGG  
 TGCCCACTCCCCACCCTGCAGGACAGGGGTGTCTGTGGACACTCCACACCCAACCTCTGC  
 TACCAAGCAGGCGTCTCAGCTTTCCTCCTCTTACCCTTTCAGATACAATCACGCCAGC  
 CACGTTGTTTGAATAATTTCTTTTGGGGGGCAGCAGTTTTCTTTTAACTTAA  
 ATAAATT (SEQ ID NO:42)

**Protein Sequence for CG50817-04 ORF Start: 520 ORF Stop: 1192 Frame: 1**

Protein Sequence:

>CG50817-04-prot 224 aa

MSDEDSVCVACGSLRTAGPQAGAPSPWPWEARLMHQQLACGGALVSEEAVLTAHCFGR  
 QAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLAQPVTLGASLRPLCLPYA  
 DHHLDPGERGWVLGRARPGAGISSLTQVPVTLGPRACSRSLHAAPGGDGPILPGMVCTS  
 AVGELPSCEANQPAADRPGHSGEQENAGRQMAALLPLSSPPCHV (SEQ ID NO:43)

**Figure 17. Nucleotide and Protein Sequences for CG50817-05.****. Nucleotide sequence encoding the Peptidase-like protein of the invention.**

&gt;CG50817-05

```

CGCTGGGCCTCTGTCCTGATGCTGCTGAGCTCCCTGGTGTCTCTCGCTGGTTCTGTCTAC 60
CTGGCCTGGATCCTGTTCTTCGTGCTCTATGATTTCTGCATTGTTTGTATCACCACCTAT 120
GCTATCAACGTGAGCCTGATGTGGCTCAGTTTCCGGAAGGTCCAAGAACCCAGGGCCAA 180
CCCAAGCCTCAGGAGGGCAACACAGTCCCTGGCGAGTGGCCCTGGCAGGCCAGTGTGAGG 240
AGGCAAGGAGGCCACATCTGCAGCGGCTCCCTGGTGGCAGACACCTGGGTCCCTCACTGCT 300
GCCCCACTGCTTTGAAAAGGCAGCAGCAACAGAACTGAATTCCTGCGTGAGGGACTCAGCC 360
CCTGGGGCCGAAGAGGTGGGGGTGGCTGCCCTGCAGTTGCCAGGGCCTATAACCACTAC 420
AGCCAGGGCTCAGACCTGGCCCTGCTGCAGCTCGCCACCCACGACCCACACACCCCTC 480
TGCCTGCCCCAGCCCGCCCATCGCTTCCCCTTTGGAGCCTCCTGCTGGGCCACTGGCTGG 540
GATCAGGACACCAAGTGATGCTCCTGGGACCCCTACGCAATCTGCGCCTGCGTCTCATCAGT 600
CGCCCCACATGTAAGTGTATCTACAACCAGCTGCACCAGCGACACCTGTCCAACCCGGCC 660
CGGCCTGGGATGCTATGTGGGGGCCCCAGCCTGGGGTGCAGGGCCCCTGTCAGGGAGAT 720
TCCGGGGGGCCCTGTGCTGTGCCTCGAGCCTGACGGACACTGGGTTCAGGCTGGCATCATC 780
AGCTTTGCATCAAGCTGTGCCCAGGAGGACGCTCCTGTGCTGCTGACCAACACAGCTGCT 840
CACAGTTCCTGGCTGCAGGCTCGAGTTCAGGGGGGAGCTTTCCTGGCCCAGAGCCAGAG 900
ACCCCGGAGATGAGTGATGAGGACAGCTGTGTAGCCTGTGGATCCTTGAGGACAGCAGGT 960
CCCCAGGCAGGAGCACCTCCCCATGGCCCTGGGAGGCCAGGCTGATGCACCAGGGACAG 1020
CTGGCCTGTGGCGGAGCCCTGGTGTGAGAGGAGCGGTGCTAACTGCTGCCCACTGCTTC 1080
ATTGGGCGCCAGGCCCCAGAGGAATGGAGCGTAGGGCTGGGGACCAGACCGGAGGAGTGG 1140
GGCCTGAAGCAGCTCATCCTGCATGGAGCCTACACCCACCCTGAGGGGGGGCTACGACATG 1200
GCCCTCCTGCTGCTGGCCAGCCTGTGACACTGGGAGCCAGCCTGCGGCCCTCTGCCTG 1260
CCCTATGCTGACCAACCTGCCTGATGGGAGCGTGGCTGGGTCTGGGACGGGCCCCG 1320
CCAGGAGCAGGCATCAGCTCCCTCCAGACAGTGCCCGTGACCCTCCTGGGGCCTAGGGCC 1380
TGCAGCCGGCTGCATGCAGCTCCTGGGGGTGATGGCAGCCCTATTCTGCCGGGGATGGTG 1440
TGTACCAAGTGCTGTGGGTGAGCTGCCCAGCTGTGAGGCCAACCAACCAGCTGCTGACAGG 1500
GGACCTGGCCATTCTCAGGAACAAGAGAATGCAGGCAGGCAAATGGCATTACTGCCCTG 1560
TCCTCCCCACCCTGTCATGTGTGATTCCAGGC 1592

```

(SEQ ID NO:44)

**Protein sequence encoded by the coding sequence shown above.**

&gt;CG50817-05

```

MLLSSLVSLAGSVYLAWILFFVLYDFCIVCITTYAINVSLMWLSFRKVQEPQGQPKPQEG 60
NTVPGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAATELNSCVRDSAPGAEEV 120
GVAALQLPRAYNHYSQGSDDLALLQLAHPHTHTPLCLPQPAHRFPFGASCWATGWDQDTS 180
APGTLRLNRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQGDSGGPVL 240
CLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAFLAQSPETPEMSD 300
EDSCVACGSLRTAGPQAGAPSPWPWEARLMHQQLACGGALVSEEAVLTAHCFIGRQAP 360
EEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLCLPYADHH 420
LPDGERGWVLGRARPGAGISSLQTPVTLTGPRACSRLLHAAPGGDGPILPGMVCTSAVG 480
ELPSCEANQPAADRGPGHSGEQENAGRQMALPLSSPPCHV 521

```

(SEQ ID NO:45)

**Figure 18. Nucleotide and Protein Sequences for CG50817-06.**

**Nucleotide sequence encoding the Peptidase-like protein of the invention.**

```
>CG50817-06
AGCGACACCTGTCCAACCCGGCCCGGCTGGGATGCTATGTGGGGGCCCCCAGCCTGGGG 60
TGCAGGGCCCCCTGTCAGGGAGATTCCGGGGGCCCTGTGCTGTGCCTCGAGCCTGACGGAC 120
ACTGGGTTTCAGGCTGGCATCATCAGCTTTGCATCAAGCTGTGCCAGGAGGACGCTCCTG 180
TGCTGCTGACCAACACAGCTGCTCACAGTTCTGGCTGCAGGCTCGAGTTCAGGGGGCAG 240
CTTTCCTGGCCCAGAGCCCAGAGACCCCGGAGATGAGTGATGAGGACAGCTGTGTAGCCT 300
GTGGATCCTTGAGGACAGCAGGTCCCCAGGCAGGAGCACCTCCCCATGGCCCTGGGAGG 360
CCAGGCTGATGCACCAGGGACAGCTGGCCTGTGGCGGAGCCCTGGTGTGACAGGAGGCGG 420
TGCTAACTGCTGCCCACTGCTTCATTGGGCGCCAGGCCCCAGAGGAATGGAGCGTAGGGC 480
TGGGGACCAGACCGGAGGAGTGGGGCCTGAAGCAGCTCATCCTGCATGGAGCCTACACCC 540
ACCCTGAGGGGGGGCTACGACATGGCCCTCCTGCTGCTGGCCCAGCCTGTGACACTGGGAG 600
CCAGCCTGCGGCCCTCTGCCTGCCCTATGCTGACCACCACCTGCCTGATGGGGAGCGTG 660
GCTGGGTTCTGGGACGGGGCCCGCCAGGAGCAGGCATCAGCTCCCTCCAGACAGTGCCCG 720
TGACCCTCCTGGGGCCTAGGGCCTGCAGCCGGCTGCATGCAGCTCCTGGGGGTGATGGCA 780
GCCCTATTCTGCCGGGGATGGTGTGTACCACTGCTGTGGGTGAGCTGCCAGCTGTGAGG 840
CCAACCAACCAGCTGCTGACAGGGGACCTGGCCATTCTCAGGAACAAGAGAATGCAGGCA 900
GGCAAATGGCATTACTGCCCTGTCTCCCCACCCTGTCATGTGTGATTCCAGGCACCAG 960
GGCAGGCCCCAGAAGCCCAGCAGCTGTGGGAAGGAACCTGCCTGGGGCCACAGGTGCCAC 1020
TCCCCACCCTGCAGGACAGGGGTGTCTGTGGACACTCCACACCCAACTCTGCTACCAAG 1080
CAGGCGTCTCAGCTTTCTCCTCCTTTACCCTTTTACATACATCACGCCAGCCACGTTG 1140
TTTTGAAAATTTCTTTTTTTGGGGGGCAGCAGTTTTCTTTTTTAAACTTAAATAAATT 1200
(SEQ ID NO:46)
```

**Protein sequence encoded by the coding sequence shown above.**

```
>CG50817-06
MLCGGPQPGVQGPCQGDSGGPVLCLEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSS 60
WLQARVQGAFLAQSPETPEMSDEDSVCVACSLRTAGPQAGAPSPWPWEARLMHQQLAC 120
GGALVSEEAVLTAHCFGRQAPEEWSVGLGTRPEEWGLKQLILHGAYTHPEGGYDMALL 180
LLAQPVTLGASLRPLCLPYADHHLDPGERGWVLGRARPGAGISSLQTPVPTLLGPRACSR 240
LHAAPGGDGSPILPGMVCTSAVGELPSCEANQPAADRPGHSQEQENAGRQMALLPLSSP 300
PCHV 304
(SEQ ID NO:47)
```



**Figure 19. Nucleotide and Protein Sequences For CG51099-03.****Nucleotide sequence encoding the Serine Protease-like protein of the invention.**

```

>CG51099-03
CGGAGAGACGCAGTCGGCTGCCACCCCGGGATGGGTCGCTGGTGCCAGACCGTCGCGCGC      60
GGGCAGCGCCCCCGGACGCTGCCCCCTCCCGCGCCGGTGCCCTGCTGCTGCTGCTTCTG      120
TTGCTGAGGTCTGCAGGTTGCTGGGGCGCAGGGGAAGCCCCGGGGCGCTGTCCACTGCT      180
GATCCCGCCGACCAGAGCGTCCAGTGTGTCCCCAAGGCCACCTGTCTTCCAGCCGGCCT      240
CGCCTTCTCTGGCAGACCCCGACCACCCAGACACTGCCCTCGACCACCATGGAGACCCAA      300
TTCCCAAGTTTCTGAAGGCAAAGTCGACCCATACCGCTCCTGTGGCTTTTCCTACGAGCAG      360
GACCCCAACCTCAGGGACCCAGAAGCCGTGGCTCGGCGGTGGCCCTGGATGGTCAGCGTG      420
CGGGCCAATGGCACACACATCTGTGCCGGCACCATCATTTGCCCTCCAGTGGGTGCTGACT      480
GTGGCCCACTGCCCTGATCTGGCGTGATGTTATCTACTCAGTGAGGGTGGGGAGTCCGTGG      540
ATTGACCAGATGACGCAGACCGCCTCCGATGTCCCGGTGCTCCAGGTCATCATGCATAGC      600
AGGTACCGGGCCCAGCGGTTCTGGTCTTGGGTGGGGCCAGGCCAACGACATCGGCCCTCCTC      660
AAGCTCAAGCAGGAACCTCAAGTACAGCAATTACGTGCGGCCCATCTGCCCTGCCCTGGCACG      720
GACTATGTGTTGAAGGACCATTCCTCGCTGCACTGTGACGGGTGGGGACTTTCCAAGGCT      780
GACGGCATGTGGCCTCAGTTCCGGACCATTCAGGAGAAGGAAGTCATCATCCTGAACAAC      840
AAAGAGTGTGACAATTTCTACCACAACCTTCACCAAAATCCCCACTCTGGTTCAGATCATC      900
AAGTCCCAGATGATGTGTGCGGAGGACACCCACAGGGAGAAGTTCTGCTATGAGCTAACT      960
GGAGAGCCCTTGGTCTGCTCCATGGAGGGCACGTGGTACCTGGTGGGATTGGTGAGCTGG      1020
GGTGCAGGCTGCCAGAAGAGCGAGGCCCCACCCATCTACCTACAGGTCTCCTCCTACCAA      1080
CACTGGATCTGGGACTGCCCTCAACGGGCAGGCCCTGGCCCTGCCAGCCCCATCCAGGACC      1140
CTGCTCCTGGCACTCCCACTGCCCTCAGCCTCCTTGCTGCCCTCTGACTCTGTGTGCC      1200
TCCCTCACTTGTGA
(SEQ ID NO:48)
1214

```

**Protein sequence encoded by the nucleotide sequence shown above.**

```

>CG51099-03
MGRWCQTVARGQRPRTSAPSRAGALLLLLLLLRSAGCWGAGEAPGALSTADPADQSVQCV      60
PKATCPSSRPRLWQPTTQTLPTTMMETQFPVSEKVDPYRSCGFSYEQDPTLRDPEAV      120
ARRWPWMVSVRANGTHICAGTIIASQWVLTVAHCLIWRDVIYSVRVGSPWIDQMTQTASD      180
VPVLQVIMHSRYRAQRFWSWVGQANDIGLLKLKQELKYSNYVRPICLPGTDYVLKDH SRC      240
TVTGWGLSKADGMWPQFRTIQEKEVILNNKECDNFYHNFTKIPTLVQIIKSQMMCAEDT      300
HREKFCYELTGEPLVCSMEGTWYLVGLVSWGAGCQKSEAPPIYLQVSSYQHWIWDCLNGQ      360
ALALPAPSRTLLLALPLPLSLLAAL
385 (SEQ ID NO:49)

```

**Figure 20. Nucleotide and Protein Sequences For CG57051-04.**

Nucleotide sequence encoding the Angiopoietin-like protein, CG57051-04.

```
>CG57051-04
TGGGGATCCTCACACGACTGTGATCCGATTCTTTCCAGCGGGCTTCTGCAACCAAGCGGGT 60
CTTACCCCGGGTCCCTCCGCGTCTCCAGTCTCGCACCTGGAACCCCAACGTCCCCGAGAG 120
TCCCGAATCCCCGCTCCCAGGCTACCTAAGAGGATGAGCGGTGCTCCGACGGCCGGGGC 180
AGCCCTGATGCTCTGCGCCGCCACCGCCGTGCTACTGAGCGCTAGATCTGGACCCGTGCA 240
GTCCAAGTCGCCGCGCTTTGCGTCTGGGACGAGATGAATGTCCTGGCGCACGGACTCCT 300
GCAGCTCGGCCAGGGGCTGCGCGAACACGCGGAGCGCACCCGCAGTCAGCTGAGCGCGCT 360
GGAGCGGCGCCTGAGCGCGTGC GGGTCCGCTGTCAGGGAACCGAGGGGTCCACCGACCT 420
CCCGTTAGCCCTGAGAGCCGGGTGGACCCTGAGGTCCTTCACAGCCTGCAGACACAAC 480
CAAGGCTCAGAACAGCAGGATCCAGCAACTCTTCCACAAGGTGGCCAGCAGCAGCGGCA 540
CCTGGAGAAGCAGCACCTGCGAATTCAGCATCTGCAAAGCCAGTTTGGCCTCCTGGACCA 600
CAAGCACCTAGACCATGAGGTGGCCAAGCCTGCCCCAAGAAAGAGGCTGCCCGAGATGGC 660
CCAGCCAGTTGACCCGGCTCACAATGTCAGCCGCCTGCACCGAGGCTGGTGGTTTGGCAC 720
CTGCAGCCATTCCAACCTCAACGGCCAGTACTTCCGCTCCATCCCACAGCAGCGGCAGAA 780
GCTTAAGAAGGGAATCTTCTGGAAGACCTGGCGGGGCCGCTACTACCCGCTGCAGGCCAC 840
CACCATGTTGATCCAGCCATGGCAGCAGAGGCAGCCTCCTAGCGTCTCTGGCTGGGCCTG 900
GTCCAGGCCACGAAAGACGGTGACTCTTGGCTCTG 937 (SEQ ID NO:50)
```

**Protein sequence encoded by the nucleotide sequence shown above.**

```
>CG57051-04
MSGAPTAGAALMLCAATAVLLSARSGPVQSKSPRFASWDEMNVLAHGLLQLGQGLREHAE 60
RTRSQLSALERRLSACGSACQGTEGSTDLPLAPESRVDPEVLHSLQTQLKAQNSRIQQLF 120
HKVAQQQRHLEKQHLRIQHLQSQFGLLDHKHLDHEVAKPARRKRLPEMAQPVDPAHNVSR 180
LHRGWWFGTCSHSNLNGQYFRSIPQQRQKLKKGIFWKTWRGRYYPLQATTMLIQPMAAEA 240
AS 242 (SEQ ID NO:51)
```

**Figure 21. Nucleotide and Protein Sequences For CG57051-05.**

Nucleotide sequence encoding the Angiopoietin-like protein, CG57051-05.

```
>CG57051-05
CTTCGTCTCCAGTCCTCGCACCTGGAACCCCAACGTCCCCGAGAGTCCCCGAATCCCCGC    60
TCCCAGGCTACCTAAGAGGATGAGCGGCGCTCCGACGGCCGGGGCAGCCCTGATGCTCTG    120
CGCCGCCACCGCGTGCTACTGAGCGCTCAGGGCGGACCCGTGCAGTCCAAGTCGCCGCG    180
CTTTGCGTCCTGGGACGAGATGAATGTCTGGCGCACGGACTCTGCAGCTCGGCCAGGG    240
GCTGCGCGAACACGCGGAGCGCACCCGCAGTCAGCTGAGCGCGCTGGAGCGGCGCCTGAG    300
CGCGTGCGGGTCCGCGCTGTCAAGGAACCGAGGGGTCCACCGACCTCCCGTTAGCCCCCTGA    360
GAGCCGGGTGGACCTGAGGTCCTTCACAGCCTGCAGACACAACCTCAAGGCTCAGAACAG    420
CAGGATCCAGCAACTCTTCCACAAGGTGGCCAGCAGCAGCGGCACCTGGAGAAGCAGCA    480
CCTGCGAATTCAGCATCTGCAAAGCCAGTTTGGCCTCCTGGACCACAAGCACCTAGACCA    540
TGAGGGTGGCAAGCCTGCCGAAGAAAGAGGCTGCCCGAGATGGCCAGCCAGTTGACCC    600
GGCTCACAATGTGAGCCGCTGCACCATGGAGGCTGGACAGTAATTCAGAGGCGCCACGA    660
TGGCTCAGTGGACTTCAACCGGCCCTGGGAAGCCTACAAGGCGGGGTTTGGGGATCCCCA    720
CGGCAGATTCTGGCTGGGTCTGGAGAAGGTGCATAGCATCATGGGGGACCGCAACAGCCG    780
CCTGGCCGTGCAGCTGCGGGACTGGGATGGCAACGCCGAGTTGCTGCAGTTCTCCGTGCA    840
CCTGGGTGGCGAGGACACGGCCTATAGCCTGCAGCTCACTGCACCCGTGGCCGCCAGCT    900
GGGCGCCACCACCGTCCCACCCAGCGGCTCTCCGTACCCTTCTCCACTTGGGACCAGGA    960
TCACGACCTCCGCAGGGACAAGAACTGCGCCAAGAGCCTCTCTGGAGGCTGGTGGTTTGG    1020
CACCTGCAGCCATTCCAACCTCAACGGCCAGTACTTCCGCTCCATCCCACAGCAGCGGCA    1080
GAAGCTTAAGAAGGGAATCTTCTGGAAGACCTGGCGGGGCCGCTACTACCCGCTGCAGGC    1140
CACCACCATGTTGATCCAGCCCATGGCAGCAGAGGCAGCCTCCTAGCGTCCTGGCTGGGC    1200
CTGGTCCCAGGCCCACGAAAGAGGTGACTCTTGGCTCTG    1239 (SEQ ID NO:52)
```

Protein sequence for Angiopoietin-like protein, CG57051-05.

```
>CG57051-05
MSGAPTAGAALMLCAATAVLLSAQGGPVQSKSPRFASWDEMNVLAHGLLQLGQGLREHAE    60
RTRSQLSALERRLSACGSACQTEGSTDLPLAPESRVDPEVLHSLQTQLKAQNSRIQQLF    120
HKVAQQQRHLEKQHLRIQHLQSQFGLLDHKHLDHEGGKPARRKRLPEMAQPVDPAHNVSR    180
LHHGWTVIQRRHDGSVDFNRPWEAYKAGFGDPHGEFWLGLKVVHSMGDRNSRLAVQLR    240
DWDGNAELLQFSVHLGGEDTAYSLQLTAPVAGQLGATTVPVPSGLSVPFSTWDQDHLRRD    300
KNC AKSLSGGWWFGTCSHSLNLNGQYFRSIPQQRQKLKKGIFWKTRGRYYPLQATTMLIQ    360
PMAAEAAS    368 (SEQ ID NO:53)
```

**Figure 22. Nucleotide and Protein Sequences For CG57051-02.****Nucleotide sequence encoding the Angiopoietin-like protein of the invention.**

```

>CG57051_02
TGCGGATCCTCACACGACTGTGATCCGATTCTTTCCAGCGGCTTCTGCAACCAAGCGGGT    60
CTTACCCCGCGTCTCCGCGTCTCCAGTCCTCGCACCTGGAACCCCAACGTCCCGGAGAG    120
TCCCGAATCCCGCTCCAGGCTACCTAAGAGGATGAGCGGTGCTCCGACGGCCGGGGC    180
AGCCCTGATGCTCTGCGCCGCCACCGCCGTGCTACTGAGCGCTAGATCTGGACCCGTGCA    240
GTCCAAGTCGCCGCGCTTTGCGTCTGGGACGAGATGAATGTCCTGGCGCACGGACTCCT    300
GCAGCTCGGCCAGGGGCTGCGCGAACACGCGGAGCGCACCCGCAGTCAGCTGAGCGCGCT    360
GGAGCGGCGCCTGAGCGCGTGGGGTCCGCTGTGTCAGGGAACCGAGGGGTCCACCGACCT    420
CCCGTTAGCCCCCTGAGAGCCGGGTGGACCCCTGAGGTCTTTCACAGCCTGCAGACACAAC    480
CAAGGCTCAGAACAGCAGGATCCAGCAACTCTTCCACAAGGTGGCCAGCAGCAGCGGCA    540
CCTGGAGAAGCAGCACCTGCGAATTTCAGCATCTGCAAAGCCAGTTTGGCCTCCTGGACCA    600
CAAGCACCTAGACATGAGGTGGCCAAACCTGCCCGAAGAAAGAGGCTGCCGAGATGGC    660
CCAGCCAGTTGACCCGGCTCACAAATGTGAGCCGCTGCACCATGGAGGCTGGACAGTAAT    720
TCAGAGGCGCCACGATGGCTCAATGGACTTCAACCGGCCCTGGGAAGCCTACAAGGCGGG    780
GTTTGGGGATCCCCACGGCGAGTTCTGGCTGGGTCTGGAGAAGGTGCATAGCATCACGGG    840
GGACCGCAACAGCCGCTGGCCGTGTCAGCTGCGGGACTGGGATGGCAACGCCGAGTTGCT    900
GCAGTTCTCCGTGCACCTGGGTGGCGAGGACACGGCCTATAGCCTGCAGCTCACTGCACC    960
CGTGGCCGGCCAGCTGGGCGCCACCACCGTCCCAACCCAGCGGCCTCTCCGTACCCTTCTC    1020
CACTTGGGACCAGGATCACGACCTCCGACGGGACAAGAAGTGCAGCAAGAGCCTCTCTGC    1080
CCCATCGGTGGCTCAAAGACCTGACCATGTTCCCTCTCCCTGACCCCGGAGGAGGCTG    1140
GTGGTTTGGCACCTGCAGCCATTCCAACCTCAACGGCCAGTACTTCCGCTCCATCCCACA    1200
GCAGCGGCAGAAAGCTTAAGAAGGGAATCTTCTGGAAGACCTGGCGGGGCCGCTACTACCC    1260
GCTGCAGGCCACCACCATGTTGATCCAGCCATGGCAGCAGAGGCAGCCTCCTAG    1315
(SEQ ID NO:54)

```

**Protein sequence for CG57051-02.**

```

>CG57051_02
MSGAPTAGAALMLCAATAVLLSARSGPVQSKSPRFASWDEMNVLAHGLLQLGQGLREHAE    60
RTRSQLSALERRLSACGSACQGTGSTDLPAPESRVDPEVLHSLQTQLKAQNSRIQQLF    120
HKVAQQQRHLEKQHLRIQHLSQFGLLDHKHLDHEVAKPARRKRLPEMAQPVDPAHNVSR    180
LHHGGWTVIQRHDGSMDFNRPWEAYKAGFGDPHGEFWLGLEKVHSITGDRNSRLAVQLR    240
DWDGNAELLQFSVHLGGEDTAYSLQLTAPVAGQLGATTVPVPSGLSVPFSTWDQDHLRRD    300
KNCAKSLSAPSVAQRPDHVPSPPLTPAGGWVFGTCSHSLNNGQYFRSIPQQRQKLKKGIFW    360
KTRWRGYYPLQATTMLIQPMAAEAS    386 (SEQ ID NO:55)

```

**Figure 23. Nucleotide and Protein Sequences For CG57051-03.**

Nucleotide sequence encoding the Angiopoietin-like protein, CG57051-03.

```
>CG57051-03
CCCCGAGAGTCCCCGAATCCCCGCTCCAGGCTACCTAAGAGGATGAGCGGTGCTCCGAC    60
GGCCGGGGCAGCCCTGATGCTCTGCGCCGCCACCGCCGTGCTACTGAGCGCTCAGGGCGG    120
ACCCGTGCAGTCCAAGTCGCCGCGCTTTGCGTCTGGGACGAGATGAATGTCCTGGCGCA    180
CGGACTCCTGCAGTCTGGCCAGGGGCTGCGCGAACACGCGGAGCGCACCCGAGTCAGCT    240
GAGCGCGCTGGAGCGGCGCCTGAGCGCGTGCGGGTCCGCTGTGAGGGAACCGAGGGGTC    300
CACCGACCTCCCGTTAGCCCCCTGAGAGCCGGGTGGACCCCTGAGGTCCTTCACAGCCTGCA    360
GACACAACCTCAAGGCTCAGAACAGCAGGATCCAGCAACTCTCCACAAGGTGGCCAGCA    420
GCAGCGGCACCTGGAGAAGCAGCACCTGCGAATTCAGCATCTGCAAAGCCAGTTTGGCCT    480
CCTGGACCACAAGCACCTAGACCATGAGGTGGCCAAGCCTGCCCAAGAAAGAGGCTGCC    540
CGAGATGGCCCAGCCAGTTGACCCGGCTCACATGTGAGCCGCTGCACCATGGAGGCTG    600
GACAGTAATTCAGAGGCGCCACGATGGCTCAGTGGACTTCAACCGGCCCTGGGAAGCCTA    660
CAAGCGGGGTTTGGGGATCCCCACGGCGAGTTCTGGCTGGGTCTGGAGAAGGTCCATAG    720
CATCACGGGGGACCGCAACAGCCGCTGGCCGTGCAGCTGCGGGACTGGGATGACAACGC    780
CGAGTTGCTGCAGTTCTCCGTGCACCTGGGTGGCGAGGACACGGCCTATAGCCTGCAGCT    840
CACTGCACCCGTGGCCGGCCAGCTGGGCGCCACCACCGTCCCACCCAGCGGCCTCTCCGT    900
ACCTTCCCCACTTGGGACCAGGATCACGACCTCCGAGGGACAAGAAGTGGCCAAGAG    960
CCTCTCTGGAGGCTGGTGGTTTGGCACCTGCAGCCATTCCAACCTCAACGGCCAGTACTT    1020
CCGCTCCATCCCACAGCAGCGGAGAGCTTAAGAAGGGAATCTTCTGGAAGACCTGGCG    1080
GGGCCGCTACTACCCGCTGCAGGCCACCACCATGTTGATCCAGCCCATGGCAGCAGAGGC    1140
AGCCTCCTAG    1150 (SEQ ID NO:56)
```

Protein sequence for CG57051-03.

```
>CG57051-03
MSGAPTAGAALMLCAATAVLLSAQGGPVQSKSPRFASWDEMNVLAHGLLQLGQGLREHAE    60
RTRSQLSALERRLSACGSACQTEGSTDLPLAPESRVDPEVLHSLQTQLKAQNSRIQQLF    120
HKVAQQQRHLEKQHLRIQHLQSQFGLLDHKHLDHEVAKPARRKRLPEMAQPVDPAHNVSR    180
LHHGGWTVIQRHDGSVDFNRPWEAYKAGFGDPHGEFWLGLEKVHSITGDRNSRLAVQLR    240
DWDDNAELLQFSVHLGGEDTAYSLQLTAPVAGQLGATTVPVPSGLSVPFPTWDQDHLRRD    300
KNCAKSLSGGWVFGTCSHNSLNGQYFRSIPQQRQKLKKGIFWKTWRGRYYPLQATTMLIQ    360
PMAAEAAS    368 (SEQ ID NO:57)
```